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Figures

Figure 1.

1 AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTGG GCTTGAAGAC CCAGAAGATG
TTTTACATAC CTATGTTGAA TGCAAACCTAC TTTCTAAACC CGAACTTCTG GGTCTTCTAC

61 ACATATGCAA GTATGATTTT GTAGAAGTTG AGGAACCCAG TGATGGAAGT ATATTAGGGC
TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC ACTACCTTGA TATAATCCCG

121 GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTC TAAAGGAAAT CAAATTAGGA
CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG ATTTCCTTTA GTTAAATCCT

+1 MetAsn IlePheLeu LeuAsnLeuLeu ThrGluGlu ValArgLeu
]-----

181 TAAGATTGT ATCTGATGAA TATTTTCCTT CTGAACCTTC TAACAGAGGA GGTAAGATTA
ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGAAG ATTGTCTCCT CCATTCTAAT

+1 TyrSerCysThr ProArgAsn PheSerVal SerIleArgGlu GluLeuLys ArgThrAsp

241 TACAGCTGCA CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAAGTAAA GAGAACCGAT
ATGTCGACGT GTGGAGCATT GAAGAGTCAC AGGTATTCCC TTCTTGATTT CTCTTGGCTA

+1 ThrIlePheTrp ProGlyCys LeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys

301 ACCATTTTCT GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAAGTG TGCTGTGTGT
TGTTAAAGA CCGGTCCAAC AGAGGACCAA TTTGCGACAC CACCTTGAC ACGGACAACA

+1 LeuHisAsnCys AsnGluCys GlnCysVal ProSerLysVal ThrLysLys TyrHisGlu

361 CTCCACAATT GCAATGAATG TCAATGTGTC CCAAGCAAAG TTAATAAAA ATACCACGAG
GAGGTGTTAA CGTTACTTAC AGTTACACAG GGTTCGTTTC AATGATTTT TATGGTGTCT

+1 ValLeuGlnLeu ArgProLys ThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal

421 GTCCTTCACT TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG
CAGGAAGTCA ACTCTGGTTT CTGGCCACAG TCCCCTAAGG TGTTTACTGA GTGGCTGCAC

+1 AlaLeuGluHis HisGluGlu CysAspCys ValCysArgGly SerThrGly Gly
----->

481 GCCCTGGAGC ACCATGAGGA GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG
CGGGACCTCG TGGTACTCCT CACACTGACA CACACGTCTC CTCGTGTCC TCCTATCGGC

541 CATCACCACC AGCAGCTCTT GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA
GTAGTGGTGG TCGTCGAGAA CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT

601 ACGTATGCGT TATCTCCATC CTTAATCTCA GTTGTGTTGCT TCAAGGACCT TTCATCTTCA
TGCATACGCA ATAGAGGTAG GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT

661 GGATTTACAG TGCATTCTGA AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC
CCTAAATGTC ACGTAAGACT TTCTCCTCTG TAGTTTGTCT TAATCCTCAA CACGTTGTCC

567227 "4903450

721 TCTTTTGAGA GGAGGCCTAA AGGACAGGAG AAAAGGTCTT CAATCGTGA AAGAAAATTA
AGAAAACTCT CCTCCGGATT TCCTGCTCTC TTTTCCAGAA GTTAGCACCT TTCTTTTAAT

781 AATGTTGTAT TAAATAGATC ACCAGCTAGT TTCAGAGTTA CCATGTACGT ATTCCACTAG
TTACAACATA ATTTATCTAG TGGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC

841 CTGGGTTCTG TATTTTCAGTT CTTTCGATAC GGCTTAGGGT AATGTCACTA CAGGAAAAAA
GACCCAAGAC ATAAAGTCAA GAAAGCTATG CCGAATCCCA TTACAGTCAT GTCCTTTTTT

901 ACTGTGCAAG TGAGCACCTG ATTCCGTTGC CTGCTTAAC TCTAAAGCTC CATGTCCTGG
TGACACGTTT ACTCGTGGAC TAAGGCAACG GAACGAATTG AGATTTCCAG GTACAGGACC

961 GCCTAATAATC GTATAAATC TGGATTTTTT TTTTTTTTTT TGCTCATATT CACATATGTA
CGGATTTTAG CATATTTTAG ACCTAAAAAA AAAAAAAAAA ACGAGTATAA GTGTATACAT

1021 AACCAGAACA TTCTATGTAC TACAAACCTG GTTTTTAAAA AGGAACTATG TTGCTATGAA
TTGGTCTTGT AAGATACATG ATGTTTGAC CAAAAATTTT TCCTTGATAC AACGATACTT

1081 TAAACTTGT GTCGTGCTGA TAGGACAGAC TGGATTTTTC ATATTTCTTA TTAATAATTC
AATTTGAACA CAGCACGACT ATCCTGTCTG ACCTAAAAAG TATAAGAAT AATTTTAAAG

1141 TGCCATTTAG AAGAAGAGAA CTACATTCAT GGTTTGGAAG AGATAAACCT GAAAAGAAGA
ACGGTAAATC TTCTTCTCTT GATGTAAGTA CCAAACCTTC TCTATTTGGA CTTTTCTTCT

1201 GTGGCCTTAT CTTCACTTTA TCGATAAGTC AGTTTATTG TTTTATTGTG TACATTTTAA
CACCAGGAATA GAAGTGAAAT AGCTATTGAG TCAAATAAAC AAAGTAACAC ATGTAAAAAT

1261 TATTCCTCTT TTGACATTAT AACTGTTGGC TTTTCTAATC TTGTAAATA TATCTATTTT
ATAAGAGGAA AACTGTAATA TTGACAACCG AAAAGATTAG AACAAATTTAT ATAGATAAAA

1321 TACCAAGGT ATTTAATATT CTTTTTTATG ACAACTTAGA TCACTATTT TTAGCTGGT
ATGGTTTCCA TAAATTATAA GAAAAAATAC TGTGAATCT AGTTGATAAA AATCGAACCA

1381 AAATTTTCT AAACACAATT GTTATAGCCA GAGGAACAAA GATGATATAA AATATTGTTG
TTTAAALAGA TTTGTGTTAA CAATATCGGT CTCCTTGTTT CTACTATATT TTATAACAAC

1441 CTCTGACAAA AATACATGTA TTCACTCTC GTATGGTGCT AGAGTTAGAT TAATCTGCAT
GAGACTGTTT TTATGTACAT AAAGTAAGAG CATACCAGCA TCTCAATCTA ATTAGACGTA

1501 TTTAAAAAC TGAATTGGAA TAGAATTGGT AAGTTGCAAA GACTTTTTGA AAATAATTAA
AAATTTTTG ACTTAACCTT ATCTTAACCA TTCAACGTTT CTGAAAAACT TTTATTAATT

1561 ATTATCATAT CTTCCATTCC TGTTATTGGA GATGAAAATA AAAAGCAACT TATGAAAGTA
TAATAGTATA GAAGTAAGG ACAATAACCT CTACTTTTAT TTTTCGTTGA ATACTTTCAT

1621 GACATTCAGA TCCAGCCATT ACTAACCTAT TCCTTTTTTG GGGATCTG AGCCTAGCTC
CTGTAAGTCT AGGTCGGTAA TGATTGGATA AGGAAAAAC CCCTTTAGAC TCGGATCGAG

1681 AGAAAAATCAT AAGCACCTT GAAAAAGACT TGGCAGCTTC CTGATAAAGC GTGCTGTGCT
TCITTTTGTA TTTGCTGGAA CTTTTTCTGA ACCGTCGAAG GACTATTTTC CACGACACGA

1741 GTGCAGTAGG AACACATCCT ATTTATTGTG ATGTTGTGGT TTTATTATCT TAACTCTGT
CACGTCATCC TTGTGTAGGA TAAATAACAC TACAACACCA AAATAATAGA ATTTGAGACA

1801 TCCATACACT TGTATAATA CATGGATATT TTTATGTACA GAAGTATGTC TCTTAACCG
AGGTATGGA ACATATTTAT GTACCTATAA AAATACATGT CTTCATACAG AGATTGGTC

Fig. 1 (cont.)

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1861 TTCACTTATT GTACCTGG
AAGTGAATAA CATGGACC

Fig. 1 (cont.)

Figure 2. Predicted VEGF-like protein encoded by Incyte contig of 8/12/98

1 MNIFLLNLLT EEVRLYSCTP RNFSVSIREE LKRTDTIFWP GCLLVKRCGG
51 NCACCLHNCN ECQCVPSKVT KKYHEVLQLR PKTGVRLHK SLTDVALEHH
101 EECDCVCRGS TGG

65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

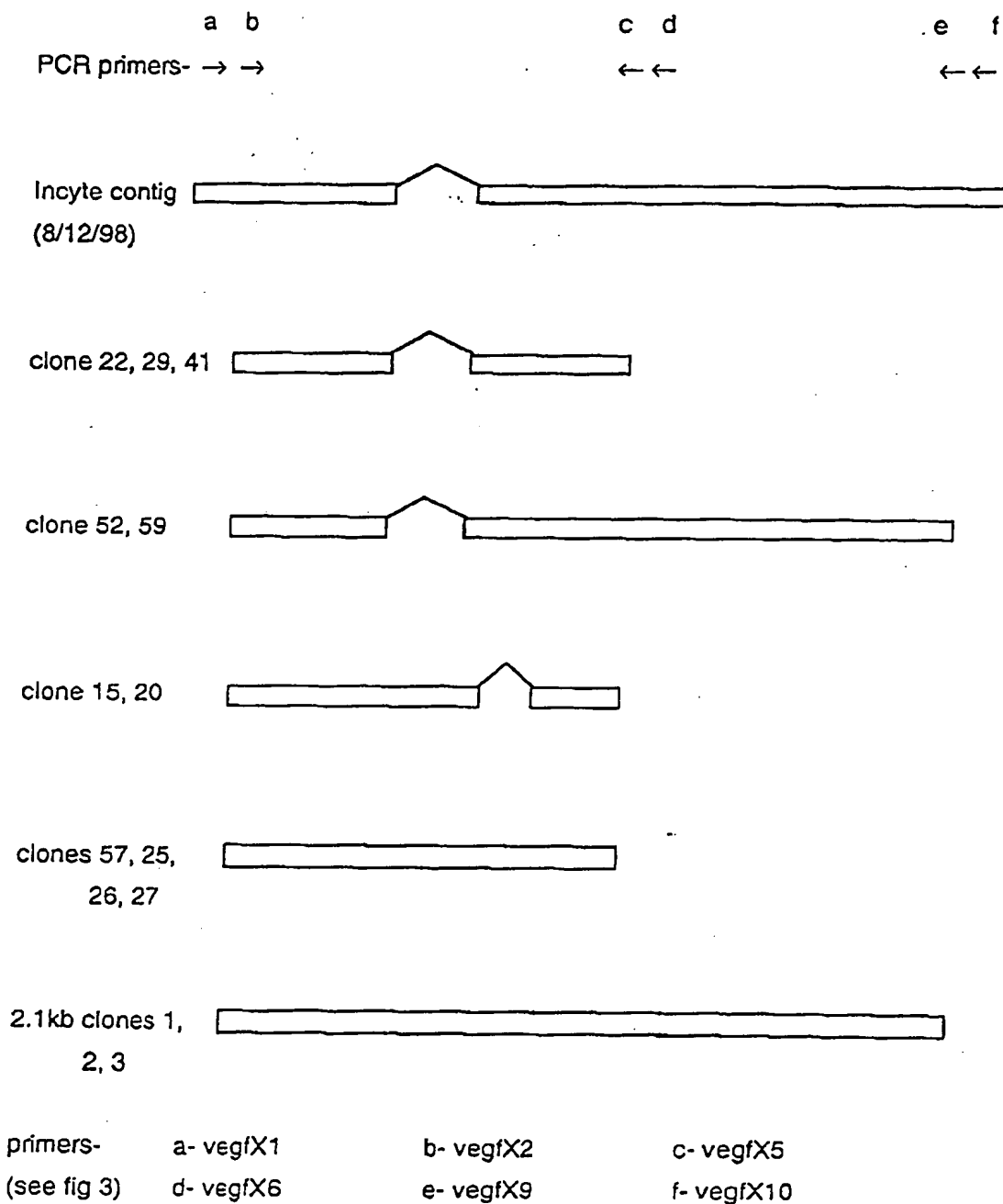
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Figure 3. PCR primers for cloning VEGF-X

vegfx1	AAAATGTATGGATACAACTTAC
vegfx2	GTTTGATGAAAGATTGGGCTTG
vegfx3	TTTCTAAAGGAAATCAAATTAG
vegfx4	GATAAGATTGTATCTGATG
vegfx5	GATGTCTCCTCTTTCAG
vegfx6	GCACAACTCCTAATTCTG
vegfx7	AGCACCTGATTCCGTTGC
vegfx8	TAGTACATAGAATGTTCTGG
vegfx9	AAGAGACATACTTCTGTAC
vegfx10	CCAGGTACAATAAGTGAAGTGA

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Figure 4. Variants Isolated by PCR



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Figure 5. VEGF-X 5' RACE primers

vegX11	CCTTAGAAATCTGTTTCCTGGTACAG
vegX12	GGAAAATATTCATCAGATACAAATCTTATCC
vegX13	GGTCCAGTGGCAAAGCTGAAGG
vegX14	CTGGTTCAAGATATCGAATAAGGTCTTCC

049544 1249
667227 4999460

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Figure 6. DNA sequence assembled from in-house clones and 5'RACE

1 TGCCAGAGCA GGTGGGCGCT TCCACCCAG TGCAGCCTTC CCCTGGCGGT GGTGAAAGAG
ACGGTCTCGT CCACCCGCGA AGGTGGGCTC ACCTCGGAAG GGGACCGCCA CCACTTTCTC

61 ACTCGGGAGT CGCTGCTTCC AAAGTGCCCG CCGTGAGTGA GCTCTCACCC CAGTCAGCCA
TGAGCCCTCA GCGACGAAGG TTTCACGGGC GGCACCTACT CGAGAGTGGG GTCAGTCGGT

+2 MetSerLeu PheGlyLeuLeu LeuLeuThr SerAlaLeu AlaGlyGlnArg GlnGlyTh
]-----

121 AATGAGCCTC TTCGGGCTTC TCCTGCTGAC ATCTGCCCTG GCCGGCCAGA GACAGGGGAC
TTACTCGGAG AAGCCCGAAG AGGACGACTG TAGACGGGAC CGGCCGGTCT CTGTCCCTG

+2 rGlnAlaGlu SerAsnLeuSer SerLysPhe GlnPheSer SerAsnLysGlu GlnAsnGl

181 TCAGGCGGAA TCCAACCTGA GTAGTAAATT CCAGTTTTC AGCAACAAGG AACAGAACGG
AGTCCGCCTT AGGTTGGACT CATCATTTAA GGTCAAAGG TCGTTGTTCC TTGTCTTGGC

+2 yValGlnAsp ProGlnHisGlu ArgIleIle ThrValSer ThrAsnGlySer IleHisSe

241 AGTACAAGAT CCTCAGCATG AGAGAAATTAT TACTGTGTCT ACTAATGGAA GTATTACACG
TCATGTTCTA GGAGTCGTAC TCTCTTAATA ATGACACAGA TGATTACCTT CATAAGTGTC

+2 rProArgPhe ProHisThrTyr ProArgAsn ThrValLeu ValTrpArgLeu ValAlaVa

301 CCCAAGGTTT CCTCATACTT ATCCAAGAAA TACGGTCTTG GTATGGAGAT TAGTAGCAGT
GGGTTCCTAA GGAGTATGAA TAGGTTCTTT ATGCCAGAAC CATACCTCTA ATCATCGTCA

+2 lGluGlnAsn ValTrpIleGln LeuThrPhe AspGluArg PheGlyLeuGlu AspProGl

361 AGAGGAAAAT GTATGGATAC AACTTACGTT TGATGAAAGA TTTGGGCTTG AAGACCCAGA
TCTCCTTTTA CATACCTATG TTGAATGCAA ACTACTTTCT AAACCCGAAC TTCTGGGTCT

+2 uAspAspIle CysLysTyrAsp PheValGlu ValGluGlu ProSerAspGly ThrIleLe

421 AGATGACATA TGCAAGTATG ATTTTGTAGA AGTTGAGGAA CCCAGTGATG GAACTATATT
TCTACTGTAT ACGTTCATAC TAAACATCT TCAACTCCTT GGGTCACTAC CTTGATATAA

+2 uGlyAspTrp CysGlySerGly ThrValPro GlyLysGln IleSerLysGly AsnGlnIl

481 AGGGCGCTGG TGTGGTCTG GTACTGTACC AGGAAAACAG ATTTCTAAAG GAAATCAAAT
TCCCGCGACC ACACCAAGAC CATGACATGG TCCTTTTGTG TAAAGATTTC CTTTAGTTTA

+2 eArgIleArg PheValSerAsp GluTyrPhe ProSerGlu ProGlyPheCys IleHisTy

541 TAGGATAGA TTTGTATCTG ATGAATATTT TCCTTCTGAA CCAGGGTCT GCATCCACTA
ATCCTATTCT AAACATAGAC TACTTATAAA AGGAAGACTT GGTCCCAAGA CGTAGGTGAT

+2 rAsnIleVal MetProGlnPhe ThrGluAla ValSerPro SerValLeuPro ProSerAl

601 CAACATGTC ATGCCACAAT TCACAGAAGC TGTGAGTCCT TCAGTGCTAC CCCCTTCAGC
GTTGTAACG TACGGTGTTA AGTGTCTTCG AACTCAGGA AGTCACGATG GGGGAAGTCC

+2 aLeuProLeu AspLeuLeuAsn AsnAlaIle ThrAlaPhe SerThrLeuGlu AspLeuIl

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Fig. 6 (cont)

661 TTGCCACTG GACCTGCTTA ATAATGCTAT AACTGCCTTT AGTACCTTGG AAGACCTTAT
AAACGGTGAC CTGGACGAAT TATTACGATA TTACGGAAA TCATGGAACC TTCTGGAATA

+2 eArgTyrLeu GluProGluArg TrpGlnLeu AspLeuGlu AspLeuTyrArg ProThrTr

721 TCGATATCTT GAACCAGAGA GATGGCAGTT GGACTTAGAA GATCTATATA GGCCAACTTG
AGCTATAGAA CTGGTCTCT CTACCGTCAA CCTGAATCTT CTAGATATAT CCGTTGAAC

+2 pGlnLeuLeu GlyLysAlaPhe ValPheGly ArgLysSer ArgValValAsp LeuAsnLe

781 GCAACTTCTT GGCAAGGCTT TTGTTTTTGG AAGAAAATCC AGAGTGGTGG ATCTGAACCT
CGTTGAAGAA CCGTTCCGAA AACAAAAACC TTCTTTTAGG TCTCACCACC TAGACTTGGA

+2 uLeuThrGlu GluValArgLeu TyrSerCys ThrProArg AsnPheSerVal SerIleAr

841 TCTAACAGAG GAGGTAAGAT TATACAGCTG CACACCTCGT AACTTCTCAG TGTCCATAAG
AGATTGTCTC CTCCATTCTA ATATGTCGAC GTGTGGAGCA TGAAGAGTC ACAGGTATTC

+2 gGluGluLeu LysArgThrAsp ThrIlePhe TrpProGly CysLeuLeuVal LysArgCy

901 GGAAGAACTA AAGAGAACCG ATACCATTTT CTGGCCAGGT TGTCTCCTGG TTAAACGCTG
CCTTCTTGAT TTCTCTTGGC TATGGTAAAA GACCGGTCCA ACAGAGGACC AATTGCGAC

+2 sGlyGlyAsn CysAlaCysCys LeuHisAsn CysAsnGlu CysGlnCysVal ProSerLy

961 TGGTGGGAAC TGTGCCTGTT GTCTCCACAA TTGCAATGAA TGTCAATGTG TCCCAAGCAA
ACCACCCTTG ACACGGACAA CAGAGGTGTT AACGTTACTT ACAGTTACAC AGGGTTCGTT

+2 sValThrLys LysTyrHisGlu ValLeuGln LeuArgPro LysThrGlyVal ArgGlyLe

1021 AGTTACTPAA AAATACCACG AGGTCTCTCA GTTGAGACCA AAGACCGGTG TCAGGGGATT
TCAATGATTT TTTATGGTGC TCCAGGAAGT CAACTCTGGT TTCTGGCCAC AGTCCCCTAA

+2 uHisLysSer LeuThrAspVal AlaLeuGlu HisHisGlu GluCysAspCys ValCysAr

1081 GCACAAATCA CTCACCGACG TGGCCCTGGA GCACCATGAG GAGTGTGACT GTGTGTGACG
CGTGTTTAGT GAGTGGCTGC ACCGGGACCT CGTGTACTC CTCACACTGA CACACACGTC

+2 gGlySerThr GlyGly
----->

1141 AGGGAGCACA GGAGGATAGC CGCATCACCA CCAGCAGCTC TTGCCCAGAG CTGTGCAGTG
TCCCTCGTGT CCTCCTATCG GCGTAGTGGT GGTGTCGAG AACGGGTCTC GACACGTCAC

1201 CAGTGGCTGA TTCTATTAGA GAACGTATGC GTTATCTCCA TCCTTAATCT CAGTTGTTTG
GTCACCGACT AAGATAATCT CTGCATACG CAATAGAGGT AGGAATTAGA GTCAACAAAC

1261 CTTCAGGAC CTTTCATCTT CAGGATTAC AGTGCATTCT GAAAGAGGAG ACATCAAACA
GAAGTTCTTG GAAAGTAGAA GTCCTAAATG TCACGTAAGA CTTTCTCTC TGTAGTTGT

1321 GAATTAGGAG TTGTGCAACA GCTCTTTTGA GAGGAGGCCT AAAGGACAGG AGAAAAGGTC
CTTAATCTC AACACGTTGT CGAGAAAACCT CTCCTCCGGA TTTCTGTCC TCTTTTCCAG

1381 TTCAATCTTG GAAAGAAAAT TAAATGTTGT ATTAAATAGA TCACCAGCTA GTTTCAGAGT
AAGTTAGAC CTTTCTTTTA ATTTACAACA TAATTTATCT AGTGGTCCAT CAAAGTCTCA

1441 TACCATGTAC GTATTCCACT AGCTGGGTTT TGTATTTTCA TTCTTTCGAT ACGGCTTAGG

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Figure 7. New Sequence + Incyte ESTs

1 ATTTGTTTAA ACCTTGGGAA ACTGGTTCAG GTCCAGGTTT TGCTTTGATC CTTTTCAAAA
TAAACAAATT TGGAACCCCTT TGACCAAGTC CAGGTCCAAA ACGAAACTAG GAAAAGTTTT

61 ACTGGAGACA CAGAAGAGGG CTTCTAGGAA AAAGTTTTGG GATGGGATTA TGTGGAACT
TGACCTCTGT GTCTTCTCCC GAAGATCCTT TTTCAAAACC CTACCCTAAT ACACCTTTGA

121 ACCCTGCGAT TCTCTGCTGC CAGAGCAGGC TCGGCGCTTC CACCCAGTG CAGCCTTCCC
TGGGACGCTA AGAGACGACG GTCTCGTCCG AGCCGCGAAG GTGGGTCAC GTCGGAAGGG

181 CTGGCGGTGG TGAAAGAGAC TCGGGAGTCG CTGCTTCCAA AGTGCCCGCC GTGAGTGAGC
GACCGCCACC ACTTTCTCTG AGCCCTCAGC GACGAAGGTT TCACGGGCGG CACTCACTCG

+2 Met SerLeuPhe GlyLeuLeu LeuLeuThrSer AlaLeuAl
|-----|

241 TCTCACCCTCA GTCAGCCAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC
AGAGTGGGGT CAGTCGGTTT ACTCGGAGAA GCCCGAAGAG GACGACTGTA GACGGGACCG

+2 aGlyGlrArg GlnGlyThrGln AlaGluSer AsnLeuSer SerLysPheGln PheSerSe

301 CGGCCAGAGA CAGGGGACTC AGGCGGAATC CAACCTGAST AGTAAATTCC AGTTTTCCAG
GCCGGTCTCT GTCCCTGAG TCCGCCTTAG GTTGGACTCA TCATTAAAGG TCAAAAGGTC

+2 rAsnLysGlu GlnTyrGlyVal GlnAspPro GlnHisGlu ArgIleIleThr ValSerTh

361 CAACAAGGAA CAGTACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC
GTTGTTCTCT GTCATGCCTC ATGTTCTAGG AGTCGTACTC TCTTAATAAT GACACAGATG

+2 rAsnGlySer IleHisSerPro ArgPhePro HisThrTyr ProArgAsnThr ValLeuVa

421 TAATGGAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT
ATTACCTTCA TAAGTGTCGG GTTCCAAAGG AGTATGAATA GGTCTTTTAT GCCAGAACCA

+2 lTrpArgLeu ValAlaValGlu GluAsnVal TrpIleGln LeuThrPheAsp GluArgPh

481 ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTACGTTTG ATGAAAGATT
TACCTCTAAT CATCGTCATC TCCTTTTACA TACCTATGTT GAATGCAAAC TACTTTCTAA

+2 eGlyLeuGlu AspProGluAsp AspIleCys LysTyrAsp PheValGluVal GluGluPr

541 TGGGCTTGA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC
ACCCGAACCT CTGGGTCTTC TACTGTATAC GTTCATACTA AAACATCTTC AACTCCTTGG

+2 oSerAspGly ThrIleLeuGly ArgTrpCys GlySerGly ThrValProGly LysGlnIl

601 CAGTGATGA ACTATATTAG GCGCTGGTG TGTTCTGGT ACTGTACCAG GAAAACAGAT
GTCACTACCT TGATATAATC CCGCGACCAC ACCAAGACCA TGACATGGTC CTTTGTCTA

+2 eSerLysGly AsnGlnIleArg IleArgPhe ValSerAsp GluTyrPhePro SerGluPr

661 TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC
AAGATTTCTT TAGTTTAAT CCTATTCTAA ACATAGACTA CTTATAAAAG GAAGACTTGG

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Fig. 7 (cont.)

+2 oGlyPheCys IleHisTyrAsn IleValMet ProGlnPhe ThrGluAlaVal SerProSe

721 AGGGTCTGCG ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG TGAGTCCTTC
TCCCAASACG TAGGTGATGT TGTAACAGTA CGGTGTTAAG TGTCTTCGAC ACTCAGGAAG

+2 rValLeuPro ProSerAlaLeu ProLeuAsp LeuLeuAsn AsnAlaIleThr AlaPheSe

781 AGTGCTACCC CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA CTGCCTTTAG
TCACGATGGG GGAAGTCGAA ACGGTGACCT GGACGAATA TTACGATATT GACGGAAATC

+2 rThrLeuGlu AspLeuIleArg TyrLeuGlu ProGluArg TrpGlnLeuAsp LeuGluAs

841 TACCTTCGAA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG ACTTAGAAGA
ATGGAACCTT CTGGAATAAG CTATAGAACT TGGTCTCTCT ACCGTCAACC TGAATCTCT

+2 pLeuTyrArg ProThrTrpGln LeuLeuGly LysAlaPhe ValPheGlyArg LysSerAr

901 TCTATAAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTGGAA GAAAATCCAG
AGATATATCC GGTGAACCG TTGAAGAACC GTTCCGAAA CAAAACCTT CTTTATAGTC

+2 gValValAsp LeuAsnLeuLeu ThrGluGlu ValArgLeu TyrSerCysThr ProArgAs

961 AGTGCTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA CACCTCGTAA
TCACCACCTA GACTTGAAG ATTGTCTCTT CCATTCTAAT ATGTCGACGT GTGGAGCATT

+2 nPheSerVal SerIleArgGlu GluLeuLys ArgThrAsp ThrIlePheTrp ProGlyCy

1021 CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT GGCCAGGTTG
GAAGAGTCAC AGGTATTCCC TTCTTGATT CTCTGGCTA TGGTAAAAGA CCGGTCCAAC

+2 sLeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys LeuHisAsnCys AsnGluCy

1081 TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCTGTGTT CTCCACAATT GCAATGAATG
AGAGGACCAA TTTGCGACAC CACCCTTGAC ACGGACAACA GAGGTGTAA CGTTACTTAC

+2 sGlnCysVal ProSerLysVal ThrLysLys TyrHisGlu ValLeuGlnLeu ArgProLy

1141 TCAATGTGTC CCAAGCAAAG TTAATAAAAA ATACCACGAG GTCCTTCAGT TGAGACCAAA
ASTTACACAG GGTTCGTTTC AATGATTTTT TATGGTGCTC CAGGAAGTCA ACTCTGGTTT

+2 sThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal AlaLeuGluHis HisGluGl

1201 GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA
CTGGCCACAG TCCCCTAACG TGTTTAGTGA GTGGCTGCAC CGGGACCTCG TGGTACTCCT

+2 uCysAspCys ValCysArgGly SerThrGly Gly
----->
1261 GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG CATCACCACC AGCAGCTCTT
CACACTGACA CACACGTCTC CCTCGTGTC TCCTATCGGC GTAGTGGTGG TCGTCGAGAA

1321 GCCCAGACCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA ACGTATGCGT TATCTCCATC
CGGGTCTTGA CACGTCACGT CACCGACTAA GATAATCTCT TGCATACGCA ATAGAGGTAG

1381 CTTAATCTCA GTTGTGTTGCT TCAAGGACCT TTCATCTTCA GGATTTACAG TGCATTCTGA
GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT CCTAATGTC ACGTAAGACT

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Fig. 7 (cont.)

1441 AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC TCTTTTGAGA GGAGGCGTAA
 TTCTCCTCTG TAGTTTGTCT TAATCCTCAA CACGTTGTCT AGAAAACTCT CCTCCGGATT
 1501 AGGACAGGAG AAAAGGTCTT CAATCGTGA AAGAAAATTA AATGTTGTAT TAAATAGATC
 TCCTGTCCTC TTTTCCAGAA GTTAGCACCT TTCTTTTAAT TTACAACATA ATTTATCTAG
 1561 ACCAGCTAST TTCAGAGTTA CCATGTACGT ATTCCACTAG CTGGGTTCTG TATTTCAAGT
 TGGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC GACCCAAGAC ATAAAGTCAA
 1621 CTTTCGATAC GGCTTAGGGT AATGTCAGTA CAGGAAAAAA ACTGTGCAAG TGAGCACCTG
 GAAAGCTATG CCGAATCCCA TTACAGTCAT GTCCTTTTTT TGACACGTC ACTCGTGGAC
 1691 ATTCCGTTGC CTTGGCTTAA CTCTAAAGCT CCATGTCCTG GGCCTAAAT CGTATAAAT
 TAAGGCAACG GAACCGAATT GAGATTTTGA GGTACAGGAC CCGGATTTTA GCATATTTTA
 1741 CTGGATTTTT TTTTTTTTTT TGGCGCATAT TCACATATGT AAACCAGAAC ATTCTATGTA
 GACCTAAAAA AAAAAAAAAA AACGCGTATA AGTGATACA TTTGGTCTTG TAAGATACAT
 1801 CTACAAACCT GGTTTTAA AAGGAACAT GTTGCTATGA ATTAACTTG TGTCATGCTG
 GATGTTTGA CCAAAATTT TCCCTTGATA CAACGATACT TAATTTGAAC ACAGTACGAC
 1861 ATAGGACAGA CTGGATTTTT CATATTTCTT ATTAAATTT CTGCCATTTA GAAGAAGAGA
 TATCCTGCT GACCTAAAAA GTATAAGAA TAATTTTAA GACGGTAAAT CTTCTCTCT
 1921 ACTACATCA TGGTTTGGAA GAGATAAACC TGAAAAGAAG AGTGGCCTTA TCTTCACTTT
 TGATGTAAGT ACCAAACCTT CTCTATTGG ACTTTCTTC TCACCGGAAT AGAAGTGAAA
 1981 ATCGATAAGT CAGTTTATTT GTTTCATTGT GTACATTTTT ATATTCTCCT TTTGACATTA
 TAGCTATCA GTCAATAAA CAAAGTAACA CATGTAAAA TATAAGAGGA AAAGTGAAT
 2041 TAACTGTTGG CTTTCTAAT CTGTAAAT ATATCTATTT TTACCAAAGG TATTTAATAT
 ATTGACAACC GAAAAGATTA GAACAATTTA TATAGATAAA AATGGTTTCC ATAAATTATA
 2101 TCTTTTTTAT GACAACTTAG ATCAACTATT TTTAGCTTGG TAAATTTTTC TAAACACAAT
 AGAAAAATA CTGTTGAATC TAGTTGATAA AAATCGAACC ATTTAAAAAG ATTTGTGTTA
 2161 TGTTATATCC AGAGGAACAA AGATGATATA AAATATTGTT GCTCTGACAA AAATACATGT
 ACAATATCGG TCTCCTTGT TCTACTATAT TTTATAACAA CGAGACTGTT TTTATGTACA
 2221 ATTCATTCT CGTAGGTGC TAGAGTTAGA TTAATCTGCA TTTAAAAAA CTGAATTGGA
 TAAAGTAAGA GCATACCACG ATCTCAATCT AATTAGACGT AAAATTTTTT GACTTAACCT
 2281 ATAGAATTGG TAAGTTGCAA AGACTTTTTG AAAATAATTA AATTATCATA TCTTCCATTC
 TATCTTAACC ATTCAACGTT TCTGAAAAAC TTTTATTAAT TTAATAGTAT AGAAGGTAAG
 2341 CTGTTATTGG AGATGAAAAT AAAAGCAAC TTATGAAAGT AGACATTGAG ATCCAGCCAT
 GACAATAACC TCTACTTTTA TTTTTCGTTG AATACTTTCA TCTGTAAGTC TAGGTCGGTA
 2401 TACTAACCTA TTCCTTTTTT GGGGAAATCT GAGCCTAGCT CAGAAAAACA TAAAGCACCT
 ATGATTGGAT AAGGAAAAAA CCCCTTTAGA CTCGGATCGA GTCTTTTTGT ATTTCTGGA
 2461 TGAAAAAAGC TTGGCAGCTT CCTGATAAAG CGTGCTGTGC TGTGCACTAG GAACACATCC
 ACTTTTTCTG AACCGTCGAA GGAATTTTC GCACGACACG ACACGTCATC CTTGTGTAGG
 2521 TATTTATGTT GATGTTGTGG TTTTATTATC TTAAGCTCTG TTCCATACAC TTGTATAAAT
 ATAAATAACA CTACAACACC AAAATAATAG AATTTGAGAC AAGGTATGTG AACATATTTA

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Fig. 7. (cont.)

2581 ACATGGATAT TTTTATGTAC AGAAGTATGT CTCTTAACCA GTTCACTTAT TGTACTCTGG
TGTACCTATA AAAATACATG TCTTCATACA GAGAATTGGT CAAGTGAATA ACATGAGACC

2641 CAATTTAAAA GAAAATCAGT AAAATATTTT GCTTGTAATA TGCTTAATAT CGTGCCTAGG
GTTAAATTTT CTTTATGTCA TTTTATAAAA CGAACATTTT ACGAATTATA GCACGGATCC

2701 TTATGTGGTG ACTATTTGAA TCAAAAATGT ATTGAATCAT CAAATAAAG AATGTGGCTA
AATACACCAC TGATAAACTT AGTTTTTACA TAACTTAGTA GTTATTTTC TTACACCGAT

2761 TTTTGGGGAG AAAATT
AAAACCCCTC TTCTAA

667271 4499450

Figure 8. Additional oligonucleotides used for amplification of entire coding region

5'-1	TTTGTTTAAACCTTGGGAAACTGG
5'-2	GTCCAGGTTTTGCTTTGATCC

65 70 75 80 85 90 95 100

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Figure 9. DNA Sequence Of Clones 4 & 7, Identical Clones Containing The Entire Open Reading Frame

```

1  TTTGTTTAAA CCTTGGGAAA CTGGTTCAGG TCCAGGTTTT GCTTTGATCC TTTCAAAAA
   AAACAAATTT GGAACCCCTT GACCAAGTCC AGGTCCAAAA CGAAACTAGG AAAAGTTTTT

61  CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT GGAAACTACC
   GACCTCTGTG TCTTCTCCCG AGATCCTTTT TCAAAACCTA CCCTAATACA CCTTTGATGG

121 CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCAC CCCAGTGCAG CCTTCCCCTG
   GACGCTAAGA GACGACGGTC TCGTCCGAGC CGCGAAGGTG GGGTCACGTC GGAAGGGGAC

181 GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCGCCGTG ACTGAGCTCT
   CGCCACCACT TTCTCTGAGC CCTCAGCGAC GAAGGTTTCA CGGGCGGCAC TCACTCGAGA

+2          MetSer LeuPheGly LeuLeuLeu LeuThrSerAla LeuAlaGl
   ]-----

241 CACCCCAAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG CCCTGGCCGG
   GTGGGGTCAG TCGGTTTACT CGGAGAAGCC CGAAGAGGAC GACTGTAGAC GGGACCGGCC

+2 yGlnArgGln GlyThrGlnAla GluSerAsn LeuSerSer LysPheGlnPhe SerSerAs
   -----

301 CCAGAGACAG GGGACTCAGG CGGAATCCAA CCGAGTAGT AAATTCCAGT TTCCAGCAA
   GGTCTCTGTC CCCTGAGTCC GCCTTAGGTT GGACTCATCA TTTAAGGTCA AAGGTCGTT

+2 nLysGluGln AsnGlyValGln AspProGln HisGluArg IleIleThrVal SerThrAs
   -----

361 CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG TGTCTACTAA
   GTTCCTTGTC TTGCCTCATG TTCTAGGAGT CGTACTCTCT TAATAATGAC ACAGATGATT

+2 nGlySerIle HisSerProArg PheProHis ThrTyrPro ArgAsnThrVal LeuValTr
   -----

421 TGGAAGTATT CACAGCCCAA GGTTCCTCA TACTTATCCA AGAAATACGG TCTTGGTATG
   ACCTTCATAA GTGTCGGGTT CCAAAGGAGT ATGAATAGGT TCTTTATGCC AGAACCATAC

+2 pArgLeuVal AlaValGluGlu AsnValTrp IleGlnLeu ThrPheAspGlu ArgPheGl
   -----

481 GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTGG
   CTCTAATCAT CGTCATCTCC TTTTACATAC CTATGTTGAA TGCAAACTAC TTTCTAAACC

+2 yLeuGluAsp ProGluAspAsp IleCysLys TyrAspPhe ValGluValGlu GluProSe
   -----

541 GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTAGAAGTTG AGGAACCCAG
   CGAACTTCTG GGTCTTCTAC TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC

+2 rAspGlyThr IleLeuGlyArg TrpCysGly SerGlyThr ValProGlyLys GlnIleSe
   -----

601 TGATGGAAC TATTAGGGC CTTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTC
   ACTACCTTGA TATAATCCCG CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG

+2 rLysGlyAsn GlnIleArgIle ArgPheVal SerAspGlu TyrPheProSer GluProGl
   -----

661 TAAAGGAAAT CAAATTAGCA TAAGATTGTG ATCTGATGAA TATTTTCCTT CTGAACCAGG

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Fig. 9 (cont.)

ATTTCTTTTA GTTTAATCCT ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGTGC
 +2 yPheCysIle HisTyrAsnIle ValMetPro GlnPheThr GluAlaValSer ProSerVa

 721 GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA GTCCTTCAGT
 CAAGACGTAG GTGATGTTGT AACAGTACGG TGTTAAGTGT CTTCGACACT CAGGAAGTCA
 +2 lLeuProPro SerAlaLeuPro LeuAspLeu LeuAsnAsn AlaIleThrAla PheSerTh

 781 GCTACCCCTC TCAGCTTTGC CACTGGACCT GCTTAATAAT GCTATAACTG CCTTAGTAC
 CGATGGGGGA AGTCGAAACG GTGACCTGGA CGAATTATTA CGATATTGAC GGAATCATG
 +2 rLeuGluAsp LeuIleArgTyr LeuGluPro GluArgTrp GlnLeuAspLeu GluAspLe

 841 CTTGGAAGAC CTTATTGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT TAGAAGATCT
 GAACCTTCTG GAATAAGCTA TAGAAGCTGG TCTCTCTACC GTCAACCTGA ATCTCTAGA
 +2 uTyrArgPro ThrTrpGlnLeu LeuGlyLys AlaPheVal PheGlyArgLys SerArgVa

 901 ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGT TTTGGAAGAA AATCCAGAGT
 TATATCCGGT TGAACCGTTG AAGAACCGTT CCGAAAACAA AAACCTTCTT TTAGGTCTCA
 +2 lValAspLeu AsnLeuLeuThr GluGluVal ArgLeuTyr SerCysThrPro ArgAsnPh

 961 GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC CTCGTAACCT
 CCACCTAGAC TTGGAAGATT GTCTCCTCCA TTCTAATATG TCGACGTGTG GAGCATTGAA
 +2 eSerValSer IleArgGluGlu LeuLysArg ThrAspThr IlePheTrpPro GlyCysLe

 1021 CTCAGTGTC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTTGTCT
 GAGTCACAGG TATTCCTTC TTGATTCTC TTGGCTATGG TAAAAGACCG GTCCAACAGA
 +2 uLeuValLys ArgCysGlyGly AsnCysAla CysCysLeu HisAsnCysAsn GluCysGl

 1081 CCTGGTAAA CGCTGTGGTG GGAAGTGTG CTGTTGTCTC CACAATTGCA ATGAATGTCA
 GGACCAATTT GCGACACCAC CCTTGACAGG GACAACAGAG GTGTTACGT TACTTACGT
 +2 nCysValPro SerLysValThr LysLysTyr HisGluVal LeuGlnLeuArg ProLysTh

 1141 ATGTGTCCCA AGCAAAGTTA CTAATAATA CCACGAGGTC CTTCAGTTGA GACCAAAGAC
 TACACAGGCT TCGTTTCAAT GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG
 +2 rGlyValArg GlyLeuHisLys SerLeuThr AspValAla LeuGluHisHis GluGluCy

 1201 CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC ATGAGGAGTG
 GCCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG GACCTCGTGG TACTCCTCAC
 +2 sAspCysVal CysArgGlySer ThrGlyGly
 ----->
 1261 TGACTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGCC
 ACTGACACAC ACGTCTCCCT CGTGTCTTCC TATCGGCGTA GTGGTGGTGG TCGAGAACGG
 1321 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT TCCTATCCTT
 GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA
 1381 AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG

Fig. 9 (cont.)

TTAGAGTCAA CAAACGAAGT TCCTGGAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC

1441 AGGAGACATC AACAGATT AGGAGTTGTG CAA
TCCTCTGTAG TTGTCTTAA TCCTCAACAC GTT

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Figure 10. Predicted Full-length Polypeptide Sequence

1 MSLFGLLLT SALAGQRQGT QAESNLSSKF QFSSNKEQYG VQDPQHERII
51 TVSTNGSIHS PRFPHTYPRN TVLVWRLVAV EENVWIQLTF DERFGLEDPE
101 DDICKYDFVE VEEPSDGTIL GRWCGSGTVF GKQISKGNQI RIRFVSDEYF
151 PSEPGFCIHY NIVMPQFTEA VSPSVLPESA LPLDLLNNAI TAFSTLEDLI
201 RYLEPERWQL DLEDLYRPTW QLLGKAFVFG RKSRVVDLNL LTEEVRLYSC
251 TPRNFSVSIR EELKRTDTIF WPGCLLVKRC GGNCACCLHN CNECQCVP SK
301 VTKKYHEVLQ LRPKTGVRGL HKSLTDVALE HHEECDCVCR GSTGG

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Figure 11 Alignment of VEGF-X with Other VEGFs

```

      .           20           .           40           .           60
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGF_HUMAN : .....
VEGC_HUMAN : .....
VEGD_HUMAN : .....
990126vegX : MSLEFCLLLLTSLALAGQRQCTQAESNLSSKQFSSNKEQNCVQDPQHERIITVSTNGSISKSPRFPHTYF : 6

      .           80           .           100          .           120
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGF_HUMAN : .....
VEGC_HUMAN : .....
VEGD_HUMAN : .....
990126vegX : RNTVLVWRLLVAVEENVWIQLTFDSRFGLDPEDDICKYDFVEV--EEDSDGTILGRWCGSGTVPGXCX : 13

      140          .           160          .           180          .           200
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGF_HUMAN : .....
VEGC_HUMAN : .....
VEGD_HUMAN : .....
990126vegX : SKGNQIRIRFVSDEYFPSEPGPCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRY : 20.

      .           220          .           240          .           260
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGF_HUMAN : .....
VEGC_HUMAN : .....
VEGD_HUMAN : .....
990126vegX : LEPEWQECLEDEYRPTWLLGKAPVFCRKSRYVCLNLTTEVLYSCFPANFVSIRILKRTDTI : 27.

      280          .           300          .           320          .           340
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGF_HUMAN : .....
VEGC_HUMAN : .....
VEGD_HUMAN : .....
990126vegX : WLLKXKNCALHNCNECHKVKYKXHYLQSPKTCVRCGLKXSTDALENSEED : 33.

      .           360          .           380          .           400
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGF_HUMAN : .....
VEGC_HUMAN : .....
VEGD_HUMAN : .....
990126vegX : CESTG : 34.5

      .           420          .           440          .           460
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGF_HUMAN : .....
VEGC_HUMAN : .....
VEGD_HUMAN : .....
990126vegX : ..... : 183

      480          .           500          .           520          .           540
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGF_HUMAN : .....
VEGC_HUMAN : .....
VEGD_HUMAN : .....
990126vegX : ..... : 21.5

VEGF_HUMAN : ..... : -
PLGF_HUMAN : ..... : -
VEGF_HUMAN : ..... : -
VEGC_HUMAN : ..... : 419
VEGD_HUMAN : ..... : -
990126vegX : ..... : -

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Figure 12. Variant Polypeptide Sequences

```

      *          20          *          40          *          60
FL_seq : MSLEGLLLTSALACCRGGTCARENLSSNECFSSNKEQNGVQDFCHERLLTVSTNGSIHSRRF : 63
clone41 : MSLEGLLLTSALACCRGGTCARENLSSNECFSSNKEQNGVQDFCHERLLTVSTNGSIHSRRF : 63
clone20 : MSLEGLLLTSALACCRGGTCARENLSSNECFSSNKEQNGVQDFCHERLLTVSTNGSIHSRRF : 63

      *          80          *          100         *          120
FL_seq : EHTYERNVLMRLVAVEENWVQLTFDERFGLERPEDDICKYDFVEVEEESDGTILGRHCCS : 126
clone41 : EHTYERNVLMRLVAVEENWVQLTFDERFGLERPEDDICKYDFVEVEEESDGTILGRHCCS : 126
clone20 : EHTYERNVLMRLVAVEENWVQLTFDERFGLERPEDDICKYDFVEVEEESDGTILGRHCCS : 126

      *          140         *          160         *          180
FL_seq : GTVEGKCIKGCNCIRIRFVSDEYFSESSNRGGKTIQHHS : 189
clone41 : GTVEGKCIKGCNCIRIRFVSDEYFSESSNRGGKTIQHHS : 167
clone20 : GTVEGKCIKGCNCIRIRFVSDEYFSESSNRGGKTIQHHS : 189

      *          200         *          220         *          240
FL_seq : EVRLYSCTP : 252
clone41 : ----- : -
clone20 : ----- : 243

      260          *          280          *          300          *
FL_seq : RNFVSSEELKRTDTIFWFGCLLVKRGCGNCACCLHNCNECCQVFSKVTKKYH : 315
clone41 : ----- : -
clone20 : ----- : 252

      320          *          340
FL_seq : ----- : 345
clone41 : ----- : -
clone20 : ----- : 282

```

Figure 13. Primers for Expression of VEGF-X

E.coli expression of domain-

vegX-6 AATTGGATCCGAGAGTGGTGGATCTGAACC
vegX-7 AATTGGATCCGGGAAGAAAATCCAGAGTGG
vegX-8 GGTTGAATTCATTATTTTTTAGTAACTTTGCTTGGGACAC
vegX-9 AATTGAATTCATTATCCTCCTGTGCTCCCTC

Baculovirus/insect cell expression of full-length protein-

vegbac1
AATTGGATCCGGAGTCTCACCATCACCACCATCATGAATCCAACCTGAGTAGTAAATTCC
C
vegbac2 AATTGAATTCGCTATCCTCCTGTGCTCCCTCTGC

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0444 49946

1 >3993180H1 LUNOT03 INCYTE
2 CACAAATCACTCACCGACG GGCCTGGAGCACCATGAGGNGTGTGACTGTGT GAGGAGCACAGGAGGATAGCC
3 GCATCACCACCAGCAGCTCTTGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATAGAGAACGTATGCGTTATCTCCAT
4 CCTTAATCTCAGTTGTTTGCTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAG
5 AATTAGGASTTGTGCAACAGCTCTTTGAGAGGAGGCTAAAGGACAGGAGAAAGGCTT
6 >3510192H1 CONCN0T01 INCYTE
7 TGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTT
8 TCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAAATTAGGAGTTGTGCAACAGCTCTTTGAGAG
9 GAGCCCTAAAGGACAGGAGAAAGSTCTTCAATCGTGGAAAGAAATTAATGTTGTATTAAATAGATCACCAGCTAGTT
10 TCAGAGTTACCATGTACGTATTCACCTAGCTGGGTTCTGTATT
11 >2559870H1 ADRETUT01 INCYTE
12 CACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCACGCTGGCCCTGGAGCACCA
13 TGAGGAGTGTGACTGTGTGTCAGAGGAGCAGGGGGATAGCCGCATCACCACGAGCTCTTGCCAGAGCTGTGTC
14 ACTCCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCA
15 TCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGA
16 >3979767H1 LUNGTUT08 INCYTE
17 GAGGATAGCCGCATCACCACGAGCTCTTGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
18 GTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAG
19 ACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGCCCTAAAGGACAGGAGAAAAGCTCTCAATCGTG
20 GAAAGAAATTAATGTTCTATTAAATAGACACCAGCT
21 >3980011H1 LUNGTUT08 INCYTE
22 GAGGATAGCCGCATCACCACGAGCTCTTGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
23 GTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACATGCATTCTGAAAGAGGAGA
24 CATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGCCCTAAAGGACAGGAGAAAAGCTCTCAATCGTG
25 AAAGAAAATTAAATGTTGTTATTAAATAGATCACA
26 >4825396H1 BLADDT01 INCYTE
27 GAGAACCGATACCATTTCTGCGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACGTGTCCTGTTGTCTCCACAATT
28 GCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAATACCACGAGGTCCTCAGTTGAGACCAAGACCGGTGTCT
29 ACGGATTCGACAAATCACTCACCAGCTGCGCCCTCGAGCACCATGAGGAGTGTGACTGTGTGTCAGAGCGGACACAGG
30 AGGATAGCCGCATCACCACCA
31 >3073703H1 BONEUNT01 INCYTE
32 AGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGTAAGATTATACAGCTGCACACCTCGTAACCTCTCAGT
33 GTCCATAAGGGAAGAATAAGAGAAACCGATACCATTTCTGCGCAGETTTCTCCTGGTTAAACGCTGTGGTGGGAAC
34 GTGCTGTGTCTCCACAATTGCAATGAATGTGTGCCAAGCAAAGTTACTAAAAATACCACGAGGTCCTTCAG
35 TTAGACACCAAGACCGGTGTGAGGCAATTGCAAAATCA
36 >1302516H1 PLACNOT02 INCYTE
37 AGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCTCTGAACTTCTAACAGAGGAGTAAGATTATAC
38 AGCTGCACACCTCGTAACCTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTCTGCGCAGGTTGTCT
39 CCTGGTTAAACGCTGTGGTGGAACTGTGCTGTGTCTCCACAATTGCAATGAATGTCAATGTGTGCCAAGCAAAGTT
40 ACTAAAAATACCACGAGGTC
41 >3684109H1 HZANCT01 INCYTE
42 ATTTCACTTTCAGGATTTACAGTGCATTCTGAAANAGGAGAAATCAAACANAATTAGGAGTTGTGCAACAGCTCTTTTGA
43 GAGGAGGCTTAAGGACAGGAGAAAAGGCTTCAATCGTGGAAANAAATTAATGTTGTATTAAATAGATCACCAGCTA
44 GTTTCAGAGTTACCATGTACGTATTCACCTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTGAG
45 TACAGCAAAAAAAGTGTGCAAGTGAACCTGATTCCGTTGCTTGCCTT
46 >4713188H1 BRAHCT01 INCYTE
47 CAAAGTTACTAAAAATACCACGAAGTCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCG
48 ACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGGATACCCGCATCACCACGAGCAG
49 CTCTTGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAAGCTATGCGTTATCTCCATCCTTAATCTCAGTTGT
50 TTGCT
51 >458823H1 XERANOT01 INCYTE
52 ANGAGTTGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT
53 GTTTGNTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAAATTAGGAGTTGTG
54 CAACACCTCTTTTGAGAGGAGGCCCTAAAGGNCAGGACAAAGCTCTCAATCGTGGAAAGAAATTAATGTTGTATTAA
55 ATAGATC
56 >1303909H1 PLACNOT02 INCYTE
57 AGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCTCTTCTGAACCTTCTAACAGAGGAGGTAAGATTATAC
58 AGCTGCACACCTCGTAACCTTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTCTTGCCAGGTTGTCT
59 CCTGGTTAAACGCTGTGGTGGGAACTGTGCTGTGTCTCCACAATTGCAATGAATGTCAATGTGTGCCAAG
60 >2739211H1 OVARNOT09 INCYTE
61 GTGCATTCTGAAAGAGGAGACATCAAACAGAAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGA
62 GAAAAGGCTTCAATCGTGGAAAGAAATTAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACG
63 TATTCCACTAGCTGGGTTCTGTATTTCACTTCTTCGATACGGCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAA
64 GTGAGCACCTGAT
65 >3325591H1 PTHYN0T03 INCYTE
66 TGCAACAGCTCTTTTGAGAGGAGCCCTAAAGGACAGGAGAAAAGCTTCAATCGTGGAAAGCAAATTAATGTTCTATT
67 AAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCACCTAGCTGGGTTCTGTATTTCAGTTCTTTTCGATACG
68 GCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAACCTGATTCCGTTGCTTTCGTTAACCTTAAGCNC
69 ATGTCNNGGGCNAAAAACGAAAAAT
70 >3733565H1 SYCN0S01 INCYTE
71 CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGNAAGANGAGACATCAAACAG
72 AATTAGGNGTTGTGCAAAAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGAGAAAAGCTCTNCAATCGTGAAAGNAAT
73 AAATGTTGTATNAATNGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCACCTAGCTGGGNCNGATTACGCT
74 TTCGGAACGGCTTAGGGTAATGTGTCAGTACAOGANAAAACTGTGTCAGTGAG
75 >3554223H1 SYNONOT01 INCYTE

Fig. 14

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76 ATTAAATAGATCACCAGCTTTTCAGAGTTACCATGTACGTATTCCACTAGCTTCTGTATTTCACTTCTTTTCGAT
 77 ACGGCTTAGGGTAATGTCAACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCGCTTGGCTTAACTCTAAAG
 78 CTCCATGTCTCTGGGCCTAAAATCGTATAAATCTCGATTTTTTTTTTTTTTTTTATATTACATATGTAAACCAGN
 79 ACATTCTATGTACNACAAACCTGGTTTTTAAAAAGQAAC
 80 >4507477H1 OVAR101 INCYTE
 81 GCGTACTTTTCAGACTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCACTTCTTTTCGATACGGCTTAGGCTAAT
 82 GTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCTTGCCTTAACTCTAAAGCTCCATGTCTTGGCCC
 83 TAAAATCGTATAAAATCTGGA
 84 >4163378H1 BRSTNOT32 INCYTE
 85 AATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNTCTGTATTTCACTTCTTTTCGATACG
 86 GCTTAGGGTAATGTCACTACAGGAAAAAGCTGTGCAAGTGAGCACCTGATTCCTTGCCTTAACTCTAAAGCTCC
 87 ATGTCTTGGGCCTAAAATCTATA

Fig 14 (cont'd)

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Fig. 15 (cont.)

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76 >877279H1 LUNG1ST01 INCYTE
77 CTTTTTATGACAACCTTAACTATTTTAGCTTGGTAAATTTTCTAAAC TGTATAGCCAGAGGAACAAA
78 GATGATATAAAATATTGTGCTCTCAAAAAATACATGTATTTCATTCTCGTATC TAGAGTTAGATTAATCTGCAT
79 TTTAAAAAACTCAATTGGAATAGAAATGGTAAGTTGCAAGGCTTTTGAATAATTAATATCATATCTTCCATTCC
80 TGTATTGGNGG
81 >4713188H1 BRAINCT01 INCYTE
82 CAAAGCTTACTAAAAAATACCACGAGCTCCTTCAGTTACACCAAAGACCGGTGTCAGGGGATTCCACAAATCCTCACC
83 ACGTGGCCCTGGACCATGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATCACCACGAGCG
84 CTCTTGGCCAGAGCTGTGTCAGTGCAGTGCCTGATTCTATTAGAGAACGATGCGTTATCTCCATCCTTAATCTCAGTTGT
85 TTGCT
86 >2171082H1 ENDCNOT03 INCYTE
87 AGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTATCGATAAGTCAGTTTATTTGTTTCATTOTGTACATTTTA
88 TATTCTCCTTTTGACATTATAACTGCTGGCTTTTCTAATCTTGTAAATATATCTATTTTACCAGGATTTAATATT
89 CTTTTTATGACAACCTTAGATCAACTATTTTAGCTTGGTAAATTTTCTAAACACAATTGTATAGCCAGAGGAACAAA
90 GATGA
91 >875860H1 LUNGAST01 INCYTE
92 CTGGATTTTTCATATTCTTATTAAAAATTTCTGCCATTTAGAGAAGAGAACTACATTCATGGTTTGAAGAGATAAACC
93 TGAAAAGAAGAGTGGCCTTATCTTCACTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATTCTCCT
94 TTTGACATTATAACTGTTGGCTTTCTAATCTTGTAAATATATCTATTTTACCAGGATTTAATATTCTTTTAT
95 GAC
96 >706168H1 SYNORAT04 INCYTE
97 GCTCATATTCACATATGTAAACCGAAGCATTCTATCTACTACAAACCTGGTTTAAAAAGGANCATGTTGCTATGAAT
98 TAAACTTGTGTCGTCGATAGSACAGACTGGATTTTTCATATTTCTTATTAAAAATTTCTGCCATTTAGAAGAAGAGAAC
99 TACATTCATGGTTTGAAGAGATAAACCCTGAAAAGAAGAGTGGCCTTATCTTCANTTTATCGATAAGTCAGTTTATTGT
100 TTCA
101 >459223H1 KERPACT01 INCYTE
102 ANGAGTTGCCAGAGCTGTSCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT
103 GTTGTNTTCAAGGACCTTTTCACTCTCAGGATTTACAGTGCATTCTGAAGSAGGAGACATCAACAGAAATAGGAGTTGTG
104 CAAAGCTCTTTTGACAGGAGGCTTAAAGGNCAGGAGAAAAGGCTCTTCAATCGTGAAGAAAATTAATGTTGTATTAA
105 ATAGATC
106 >538436H1 LNCN0T02 INCYTE
107 AAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTTCATTCTCGTATGGTGTAGAGTTAGATTAACTG
108 CATTTTAAAAAATGAATTGGAATAGAATTGGTAAGTTGCAAGACTTTTGAAGAAATTAATAATTAATCATATCTTCCAT
109 TCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAGTAGACATTCAGATCCAGCCATTACTAACCTAT
110 >1303909H1 FLACNOT07 INCYTE
111 AGGAATCAAAATTAGGATAAAGATTGTATCTGATGAATATTTTCTTCTGAACTTCTAACAGAGGAGGTAAAGTTATAC
112 AGCTGCACACCTCGTAACCTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTCTTGGCCAGGTTGTCT
113 CCTGTTAAACGCTGTGGTGGGAACCTGTGCTGCTTCCACAATTCGAATGAATGTCAATGTGTGCCCAAG
114 >2739211H1 OVARNOT09 INCYTE
115 GTGCAATCTGAAGAGGAGACATCAACAGAAATAGGAGTGTGCAACAGCTCTTTTGAGAGGAGGCTTAAAGGACAGGA
116 GAAAAGGTCTTCAATCTGTGGAAGAAAATTAATGTTGTATTAAATAGATCACCAGCTAGTTTCAAGATTACCATGTACG
117 TATTCACCTAGCTGGGTTCTGTATTTCACTTCTTTCGATACGGCTTAGGGTAATGTCAATACAGGAAAAAATCTGTCAA
118 GTGAGCACCTGAT
119 >2550343H1 LUNGUT06 INCYTE
120 TGTACATTTTATATTTCTCTTTTGACATTATAACCTGTTGCTTTTTCNAATCTTGTAAATATATCTATTTTACCAGG
121 GTATTTAATATTCTTTTATGACAACTTAGATCAACTATTTTTAGCTTGTAAATTTTCTAAACACAATTGTTATAGC
122 CAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCACTCTCGTATGGTGCTA
123 >5321148H1 PBPEN06 INCYTE
124 CACAATTGTATAGCCAGAGGAAAGATGATATAAAATATTGTTGCTCTGNCAAAAATACATGTATTTTCACTCTCGTA
125 TGGTGTAGAGTTAGATTAACTGCACTTTTAAAAAATGAATTGGAATAGAATTGGTAAGTTGCAAGACTTTTGAAGA
126 TAATTAATATCATATCTTCCATTCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAGTAAATTCAGATCCAC
127 CATTACTAAC
128 >879495H1 THYRNOT02 INCYTE
129 ATTTTCATTCTCGTATGGTGTAGAGTTAGATTAACTGCACTTTTAAAAAATGAATTGGAATAGAATTGGTAAGTTGCAA
130 AGACTTTTGAAGATAATTAATATATATCTTCCATTCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAGT
131 AGACATTGATCTCAGCCATTACTAACCTATTCCTTTTGGGGAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCT
132 TGAAGAA
133 >3325591H1 PTHYN0T03 INCYTE
134 TGCAACAGCTCTTTTGAGAGGAGGCTTAAAGGACAGGAGAAAAGGCTCTTCAATCGTGAAGAAAATTAATGTTGTATT
135 AAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCACCTAGCTGCGTTCTGTATTTCAGTTCTTCCATACG
136 GCTTAGGCTAATGTCACTACAGGAAAAAAGCTGTGCAAGTGAGCAGCTGATTCGCTTGGCTTGGCTTAACCTAAAGCNC
137 ATGTCTNNGGCNAAAANCAGAAAT
138 >543890H1 OVARNOT02 INCYTE
139 TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTCA
140 TTCTCGTATGGTCTAGATTAGATTAACTGCACTTTTAAAAAATGAATTGGAATAGAATTGGTAAGTTGCAAGACTTTTGAAGA
141 TTTGAAGATAATTAATATCATATCTTCCATTCCTGTTATTGGAGGATGAAAATAAAAGCAACTTATGGAAGTAGG
142 ACATTGAGATC
143 >3733565H1 SMCCN0501 INCYTE
144 CCTTAATCTCAGTTCTTGTCTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGNAAGANGAGACATCAACAG
145 AATTAGGNTTGTGCAAAAGCTCTTTTGAGAGGAGGCTTAAAGGACAGGAGAAAAGGCTCTNCAATCGTGGAAAGNAAT
146 AATGTTGTATTAATNGATCAGCTAGCTTTCAGACTTACCATGTACCTATTCCTACTACCTGGGNCNGTATTTCAGTCT
147 TCCGGAACCCCTTAGGGTAATGTCACTACAGGANAAGAACTGTGCAAGTGA
148 >4641939H1 PROSTM03 INCYTE
149 GTACTACAAACCTGCTTTTAAAAAGGACTATGTTGCTATGAATTAACCTGTGTCATGCTGATAGGACAGACTGGAT
150 TTTNCATATTTCTTATAAATTTCTCTCCATTTAGAGAAGAGAACTACATTCATGGTTTGGNAGAGATAAACCCTGAAAA

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226 CTTTTTAAAAAATGANTTATAGANTTCCTAAGTTGCAAAGNCNTTTGAAAATAAGTTATCAGAT
 227 >3530274H1 BLA T09 INCYTE
 228 TTCCATTCCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAAGTAGACATTATCCAGCCATTACTAACCTATT
 229 CCTTTTTTGGGGAAATCTGAGCCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAGACTTGGCAGCTTCCTGATAAAGCG
 230 TGCTGTGCTGTGCAAGTAGGAACACATCCTATTTATTGTGATGTTGTGCTTTTATTATCTAAACTCTGTTCCATACACTTG
 231 TATAAATACATGGATATTTTTTATGTACAGAAAGTATGCTCTTTAACCAGTTCA
 232 >3530249H1 BLADNOT09 INCYTE
 233 CTTCCATTCCCTGTTATTGAGATGAAAATAAAAGCAACTTATGAAAGTACACATTTCAGATCCAGCCATTACTAACCTAT
 234 TCCTTTTTTGGGGAAATCTGAGCCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAGACTTGGCAGCTTCCTGATAAAGC
 235 GTGCTGTGCTGTGCAAGTAGGAACACATCCTATTTATTGTGATGTTGTGCTTTTATTATCTAAACTCTGTTCCATACACT
 236 TGTATAAATACATGGATATTTTTTATGTACAGAAAGTATGCTCTTTAACCAGTTCACTTATTCTACCTGG
 237

Fig 15 (cont'd)

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VEGFE1	AAAATGTATGGATACAACTTAC	22
VEGFE2	GTTTGATGAAAGATTGGGCTTG	23
VEGFE3	TTTCTAAAGGAAATCAAATTAG	22
VEGFE4	GATAAGATTGTATCTGATG	20
VEGFE5	GATGTCTCCTCTTTCAG	17
VEGFE6	GCACAACTCCTAATTCTG	18
VEGFE7	AGCACCTGATTCCGTTGC	19
VEGFE8	TAGTACATAGAATGTTCTGG	20
VEGFE9	AAGAGACATACTTCTGTAC	19
VEGFE10	CCAGGTACAATAAGTGAAGTGA	21

Fig. 16

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0546644 4 12 49

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+3 M N I F L L N L L T E E V R L Y
1 AGGAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTTCCTCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC
TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAACAC TTGGAAGATT GTCTCCTCCA TTCTAATATG
+3 S C T P R N P S V S I R E E L K R T D T I F W P G C L
81 AGCTGCACAC CTCGTAACCT CTCAGTGTC ATAAGGGAAG AACTAAAGAG AACCCATACC ATTTCTGGC CAGGTTGTCT
TCGACGTGTC GAGCATTGAA GAGTCACAGG TATTCCTTC TTGATTCTC TTGGCTATGG TAAAGACCG GTCCAACAGA
-2
+3 L V K R C G G N C A C C L H N C N E C Q C V P S K V
161 CCTGGTTAAA CGCTGTGGTG GGAAGTGTG CTGTTGTCTC CACAATTCCA ATGAATGTCA ATGTGTCCCA AGCAAAGTAA
GACCAATTT GCGACACCAC CCTTGACAGG CACAACACAG GTGTTAAGCT TACTTACAGT TACACAGGCT TCGTTTCAAT
-2
+3 T K K Y H E V L Q L R P K T G V R G L H K S L T D V A
+1 V S G D C T N H S P T W P
241 CTAAAAATA CCAGGAGGTC CTTCACTTGA GACCAACAGC CGGTGTGAGG GGATTGCACA AATCACTCAC CGACGTGGCC
GATTTTAT GGTGCTCCAG GAAGTCAACT CTGTTTCTG GCCACAGTCC CTAACGTGT TTAGTGAGTG GCTGCACCG
-2
+3 L E H H E E C D C V C R G S T G G
+2 V Q P E H R R I A A S P P A A L A
+1 W S T M R S V T V C A Z G A Q E D S R I T T S S S C
321 CTGGAGCACC ATGAGGAGTG TGACTGTGTG TGCAGAGGCA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGGC
GACCTCGTGG TACTCTCAC ACTGACACAC ACCTCTCCCT CGTCTCTTC TATCGCGTA GTGGTGTGTC TCGACAACGG
+2 Q S C A V Q W L I L L E N V C V I S I L N L S C L L Q
+1 P E L C S A V A D S I R E R M R Y L H P
401 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAAGC TATGCGTTAT CTCCATCCTT AATCTCAGTT GTTGTCTTCA
GTCTCGACAC GTCACGTGAC CGACTAAGAT AATCTCTTGC ATACCCAATA GAGGTAGGAA TTAGAGTCAA CAACAGAGT
+2 G P F I F R I Y S A F
481 ACGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC AACAGAATT AGGAGTTGTG CAACAGCTCT
TCCTGGAAAG TAGAAGTCCT AAATGTCAGG TAAGACTTTC TCCTCTTAG TTGTCTTAA TCCTCAACAC GTTGTGAGA
561 TTTGAGAGGA CGCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG AAAATTAAAT GTTGTATTAA ATAGATCACC
AAACTCTCT CCGATTTC TGTCTCTT TCCAGAAGTT AGCACCTTTC TTTAATTAA CAACATAATT TATCTAGTGG
641 AGCTAGTTTC AGAGTTACCA TGACGTATT CCACTAGCTG GGTCTGTAT TTCAGTTCTT TCGATACGGC TTAGGGTAAT
TCGATCAAAG TCTCAATGGT ACATGCATAA GGTGATCGAC CCAAGACATA AAGTCAAGAA AGGTATGCCG AATCCATTA
721 GTCAGTACAG GAAAAAACT GTCAAGTGA GCACCTGATT CCGTTGCCCT GGCTTAACTC TAAAGTCCA TGTCTGGCC
CAGTCATGTC CTTTTTTTGA CAGTTTCACT CGTGGACTAA GGCAACGGAA CCGAATTGAG ATTTCAGGT ACAGGACCGG
801 CTAAATCGT ATAAATCTG GA
GATTTTAGCA TATTTAGAC CT

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Fig 17

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+3      M N I F L L N L L T E E V R L Y
1  AGGAAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTTCCTTCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC
   TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC TTGGAACATT GTCTCCTCCA TTCTAATATG
+3  S C T P R N F S V S I R E E L K R T D T I F W P G C L
81  AGCTGCACAC CTCGTAACCT CTCAGTGTCG ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTGTCT
   TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCTTC TTGATTCTC TTGGCTATGG TAAAGACCG GTCCAACAGA
-2
+3  L V K R C G G N C A C C L H N C N E C Q C V P S K V
161 CCTGGTTAAA CGCTGTGGTG GGAAGTGTG CTGTGTGTCT CACAATTGCA ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
   GACCAATTT GCGACACCAC CTTGACAGG GACAACAGAG GTGTAAAGT TACTTACAGT TACACAGGGT TCGTTTCAAT
-2
+3  T K K Y H E V L Q L R P X T G V R G L R K S L T D V A
+1      V S G D C T N H S P T W P
241 CTAAAAATA CCACGAGCTC CTTCACTGA GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC
   GATTTTMTAT GGTGTCTCAG GAAGTCAACT CTGTTTCTG GGCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG
-2
+3  L E H H E E C D C V C R G S T G G
+1      V Q R E H R R I A A S P P A A L A
321 CTGGAGCACC ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCA? CACCACCAGC AGCTCTTCCC
   GACCTCGTGG TACTCTCAC ACTEACACAC ACGTCTCCCT CCGTCTCTCC TATCGGCGTA GTGTGGTGG TCGAGAACGG
-2  Q S C A V Q W L I L L E N V C V I S I L N L S C L L Q
+1  P B L C S A V A D S I R E R M R Y L H P
401 CAGAGCTGTG CAGTGCAGTG CCGATTCTA TTAGAGAAGC TATGCTTAT CTCCATCTT AATCTCAGTT GTTGTCTCA
   GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA CAGGTAGGAA TTAGAGTCAA CAAACGAAGT
+2  G P F I F R I Y S A F
481 AGGACCTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT
   TCCTGGAAG TAGAAGTCTT AAATCTCAGG TAAGACTTTC TCCTCTGTAG TTGTCTTAA TCCTCAACAC GTTGTCTGAGA
561 TTTGAGAGGA GGCCTAAAGG ACACGAGAAA AGGTCTTCAA TCGTGGAAG AAAATTAAAT GTTGTATTAA ATAGATCACC
   AACTCTCTCT CCGGATTTC TGTCTCTTT TCCAGAGTT AGCACCTTC TTTTAATTAA CAACATAATT TATCTAGTGG
641 AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTCTGTAT TTCAGTCTT TCGATACGGC TTAGGGTAAT
   TCGATCAAAG TCTCAATGOT ACATGCATAA GGTGATCGAC CCAAGACATA AAGTCAAGAA AGCTATGCCG AATCCCATTA
721 GTCAGTACAC GAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTCCTT GGCTTAACTC TAAACCTCCA TGTCTCTGGC
   CAGTCATGTC CTTTPTTGA CACGTTCACT CCGGACTAA GGCACOGAA CCGAATTGAG ATTTCGAGGT ACAGGACCCG
801 CTAAATCGT ATAAATCTG GATTTTITN TTTTITTTG CGCATATTCA CATATGTAAA CCAGAACATT CTATGTACTA
   GATTTTAGCA TATTTTAGAC CTAAAAAAN AAAAAAAR CCGTATAAGT GTATACATT GTCTTGTAA GATACATGAT
881 CAAACCTGGT TTTTAAAAAG GAATTAAGT GCTATGAATT AAATGTGTG CGTGCTGATA GGACAGACTG GATTTTTCAT
   GTTGGACCA AAAATTTTC GTTGATCAA CGATACTTAA TTTGAACACA GCACGACTAT CCGTCTGAC CTAAAAAGTA
-3

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Fig 18

961 ATTTCTTATT AAAATTTCTG CCATTAGAA GAAGAGAACT ACATTCATGG TTGCAAGAG ATAAACCTGA AAGAGAGCT
 TAAAGATAA TTTAAAGAC GGTAAATCTT CTCTCTTGA TGTAACTACC AAACCTTCTC TATTGGACT TTTCTCTCA
 -3 -----
 1041 GGCCTTATCT TCACTTTATC GATAAGTCAG TTTATTTGTT TCATTCTGTA CATTTTATA TTCTCCTTTT GACATTATAA
 CCGAATAGA AGTGAAATAG CTATTCAGTC AAATAAACAA AGTAACACAT GTAAATATAT AAGAGGAAA CTGTAATATT
 -3 -----
 1121 CTGTGGCTT TCTAATCTT GTTAAATATA TCTATTTTAA CCAAGGTAT TTAATATTCT TTTTATGAC AACTTAGATC
 GACAACCGAA AAGATTAGAA CAATTTATAT AGATAAAAT CCTTCCATA AATTATAAGA AAAAATACG TTGAATCTAG
 1201 AACTATTTT AGCTTGTAA ATTTTCTAA ACACAATTCT TATAGCCAG GGAACAAAGA TGATATAAAA TATTGTGCT
 TTGATAAAAA TGAACCAT TAAAAGATT TGTGTTAACA ATATCGTCT CCTTGTCTT ACTATATTT ATAACAACGA
 1281 CTGACAAAAA TACATGTATT TCATTCTCGT ATGGTGCTAG AGTAGATTA ATCTGCATT TAAAAACG AATTGGAATA
 GACTGTTTT ATGTACATAA AGTAAGAGCA TACCACGATC TCAATCTAAT TAGACGTAAA ATTTTGTGAC TTAACCTTAT
 1361 GAATTGGTAA GTTGCAAGA CTTTGTGAAA ATAATTAAAT TATCATATCT TCCATTCTG TTATTGGAGA TGAAATAAA
 CTTAACCATT CAACGTTCT GAAAACTTT TATTAATTTA ATAGTATAGA AGCTAAGGAC AATAACCTCT ACTTTTATT
 1441 AAGCAACTTA TGAAGTAGA CATTGAGATC CAGCCATTAC TAACCTATTC CTTTTTGGG GAAATCTGAG CCTAGCTCAG
 TTGCTGAAT ACTTTCATCT GTAACCTAG CTCGGTAATG AITGCATAAG GAAAAACCC CTTTAGACTC GGATCGAGTC
 1521 AAAACATAA AGCACCTTGA AAAAGACTTG GCAGCTTCTT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA CACATCCTAT
 TTTTGTATT TCGTGEAACT TTCTCTGAAC CGTCGAAGGA CTATTTCGCA CGACAGGACA CGTCATCCTT GTGTAGGATA
 1601 TTATGTGAT GTTGTGTTT TATTATCTTA AACTCTGTTT CATACACTTG TATAAATACA TGGATATTT TATGTACAGA
 AATAACACTA CAACACCAA ATAATAGATT TTGAGACAAG GTATGTGAAC ATATTATGT ACCTATAAAA ATACATGTCT
 1681 ACTATGCTC TTAACCAGT CACTATTCT ACCTGG
 TCATACAGAG AATTGOTCA GTGAATAACA TGGACC

Fig 18 (cont'd)

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Figure 19. DNA and polypeptide sequence used for mammalian cell expression

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+1      m s l f g l l l l t s a l a g g r
1  GGATCCAAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC CGGCCAGAGA

+1  q g t q a e s n l s s k f q f s s n k e
61  CAGGGGACTC AGGCGGAATC CAACCTGAGT AGTAAATTC AGTTTCCAG CAACAAGGAA

+1  Q N G V Q D P Q H E R I I T V S T N G S
121  CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC TAATGGAAGT

+1  I H S P R F P H T Y P R N T V L V W R L
181  ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT ATGGAGATTA

+1  V A V E E N V W I Q L T F D E R F G L E
241  GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG ATGAAAGATT TGGGCTTGAA

+1  D P E D D I C K Y D F V E V E E P S D G
301  GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC CAGTGATGGA

+1  T I L G R W C G S G T V P G K Q I S K G
361  ACTATATTAG GGCCTGGTG TGGTCTGGT ACTGTACCAG GAAAACAGAT TTCTAAAGGA

+1  N Q I R I R F V S D E Y F P S E P G F C
421  AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC AGGGTCTGTC

+1  I H Y N I V M P Q F T E A V S P S V L P
481  ATCCACTACA ACATTGTCTAT GCCACAATTC ACAGAAGCTG TGAGTCCTTC AGTGCTACCC

+1  P S A L P L D L L N N A I T A F S T L E
541  CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA CTGCCTTTAG TACCTTGGA

+1  D L I R Y L E P E R W Q L D L E D L Y R
601  GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG ACTAGAAGA TCTATATAGG

+1  P T W Q L L G K A F V F G R K S R V V D
661  CCAACTGGC AACTTCTTGG CAAGGCTTTT GTTTTGGAA GAAATCCAG AGTGGTGGAT

+1  L N L L T E E V R L Y S C T P R N F S V
721  CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA CACCTCGTAA CTTCTCAGTG

+1  S I R E E L K R T D T I F W P G C L L V
781  TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT GGCCAGGTTG TCTCCTGGTT

+1  K R C G G N C A C C L H N C N E C Q C V
841  AAACGCTGTG GTGGGAAC TGCTGTTGT CTCCACAATT GCAATGAATG TCAATGTGTC

+1  P S K V T K K Y H E V L Q L R P K T G V
901  CCAAGCAAAG TTAATAAAAA ATACCACGAG GTCCTTCAGT TGAGACCAAA GACCGGTGTC

+1  R G L H K S L T D V A L E H H E E C D C
961  AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA GTGTGACTGT

+1  V C R G S T G G S R Q P F E G K P I P N
1021  GTGTGCAGAG GGAGCACAGG AGGATCTAGA GGGCCCTTCG AAGGTAAGCC TATCCCTAAC

+1  P L L G L D S T R T C H H H H H H
1081  CCTCTCCTCG GTCTCGATTC TACGCGTACC GGTCAATCACC ACCATCACCA TTGA

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Figure 20. DNA and polypeptide sequence used for baculovirus/insect cell expression

1 GAATTCAAAG GCCTGTATTT TACTGTTTTT GTAACAGTTT TGTAAATAAA AAACCTATAA
+3 m k f l v n v a l v f m v v y i s y i
61 ATATGAAATT CTTAGTCAAC GTTGCCCTTG TTTTATGGT CGTATACATT TCTTACATCT
+3 Y a D P E S H H H H H E S N L S S K F
121 ATGCGGATCC GAGTCTCAC CATCACCACC ATCATGAATC CAACCTGAGT AGTAAATTC
+3 Q F S S N K E Q N G V Q D P Q H E R I I
181 AGTTTCCAG CACAAGGAA CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA
+3 T V S T N G S I H S P R F P H T Y P R N
241 CTGTGTCTAC TAATGGAAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA
+3 T V L V W R L V A V E E N V W I Q L T F
301 CGGTCTTGGT ATGGAGATTA GTAGCAGTAG AGGAAATGT ATGGATACAA CTTACGTTTG
+3 D E R F G L E D P E D D I C K Y D F V E
361 ATGAAAGATT TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG
+3 V E E P S D G T I L G R W C G S G T V P
421 TTGAGGAACC CAGTGATGGA ACTATATTAG GCGCTGGTG TGGTTCTGGT ACTGTACCAG
+3 G K Q I S K G N Q I R I R F V S D E Y F
481 GAAAACAGAT TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC
+3 P S E P G F C I H Y N I V M P Q F T E A
541 CTTCTGAACC AGGTTCTGTC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG
+3 V S P S V L P P S A L P L D L L N N A I
601 TGAGTCCTTC ATGCTACCC CTTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA
+3 T A F S T L E D L I R Y L E P E R W Q L
661 CTGCCTTTAG TACCTTGGA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG
+3 D L E D L Y R P T W Q L L G K A F V F G
721 ACTTAGAAGA TCTATATAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTGGAA
+3 R K S R V V D L N L L T E E V R L Y S C
781 GAAATCCAG ATGGGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA
+3 T P R N F S V S I R E E L K R T D T I F
841 CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT
+3 W P G C L L V K R C G G N C A C C L H N
901 GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAAGTG TGCCTGTTGT CTTCCACAAT
+3 C N E C Q C V P S K V T K K Y H E V L Q
961 GCAATGAATG TCAATGTGTC CCAAGCAAAG TTAATAAAAA ATACCAGAGG GTCCTTCAGT
+3 L R P K T G V R G L H K S L T D V A L E
1021 TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAATCACT CACCGACGTG GCCCTGGAGC
+3 H H E E C D C V C R G S T G G
1081 ACCATGAGGA GTGTGACTGT GGTGTCAGAG GGAGCACAGG AGGATAGCTC TAGA

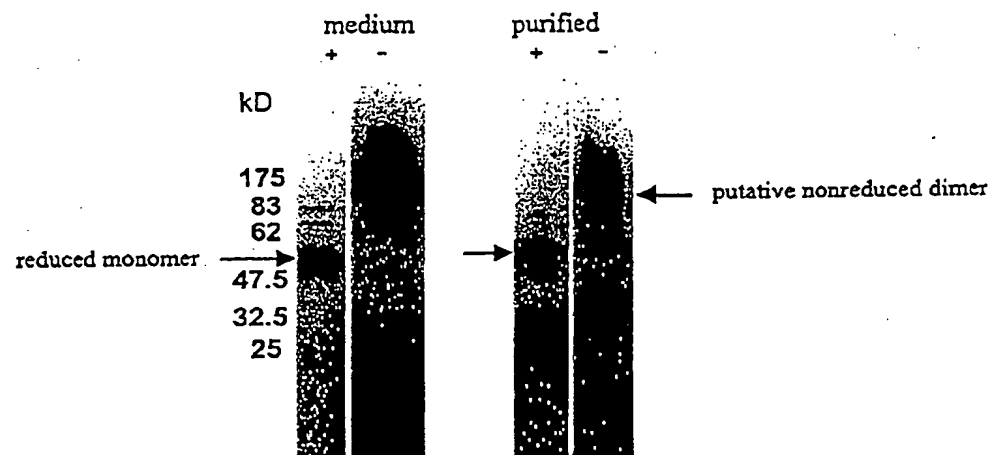
Figure 21. DNA and polypeptide sequence used for *E. coli* expression

+3 Q T N S S S N N N N N N N N N L G I
 1 CGCAGACTAA TTCGAGCTCG AACAAACAACA ACAATAACAA TAACAACAAC CTCGGGATCG
 +3 E G R I S E F E S N L S S K F Q F S S N
 61 AGGGAAGGAT TTCAGAATTC GAATCCAACC TGAGTAGTAA ATTCCAGTTT TCCAGCAACA
 +3 K E Q N G V Q D P Q H E R I I T V S T N
 121 AGGAACAGAA CGGAGTACAA GATCCTCAGC ATGAGAGAAT TATTACTGTG TCTACTAATG
 +3 G S I H S P R F P H T Y P R N T V L V W
 181 GAAGTATTCA CAGCCCAAGG TTCCTCATA CTTATCCAAG AAATACGGTC TTGGTATGGA
 +3 R L V A V E E N V W I Q L T F D E R F G
 241 GATTAGTAGC AGTAGAGGAA AATGTATGGA TACAACCTAC GTTTGATGAA AGATTGTTGGC
 +3 L E D P E D D I C K Y D F V E V E E P S
 301 TTGAAGACCC AGAAGATGAC ATATGCAAGT ATGATTTTGT AGAAGTTGAG GAACCCAGTG
 +3 D G T I L G R W C G S G T V P G K Q I S
 361 ATGGAACATAT ATTAGGGCGC TGGTGTGGTT CTGGTACTGT ACCAGGAAAA CAGATTTCTA
 +3 K G N Q I R I R F V S D E Y F P S E P G
 421 AAGGAAATCA AATTAGGATA AGATTTGTAT CTGATGAATA TTTTCTTCT GAACCAGGGT
 +3 F C I H Y N I V M P Q F T E A V S P S V
 481 TCTGCATCCA CTACAACATT GTCATGCCAC AATTCACAGA AGCTGTGAGT CCTTCAGTGC
 +3 L P P S A L P L D L L N N A I T A F S T
 541 TACCCCTTC AGCTTTGCCA CTGGACCTGC TTAATAATGC TATAACTGCC TTAGTACCT
 +3 L E D L I R Y L E P E R W Q L D L E D L
 601 TGGAAGACCT TATTGATAT CTTGAACCAG AGAGATGGCA GTTGGACTTA GAAGATCTAT
 +3 Y R P T W Q L L G K A F V F G R K S R V
 661 ATAGGCCAAC TTGGCAACTT CTGGCAAGG CTTTGTGTTT TGGAAGAAAA TCCAGAGTGG
 +3 V D L N L L T E E V R L Y S C T P R N F
 721 TGGATCTGAA CCTTCTAACA GAGGAGGTAA GATTATACAG CTGCACACCT CGTAACTTCT
 +3 S V S I R E E L K R T D T I F W P G C L
 781 CAGTGTCCAT AAGGGAAGAA CTAAAGAGAA CCGATACCAT TTTCTGGCCA GGTGTCTCTC
 +3 L V K R C G G N C A C C L H N C N E C Q
 841 TGGTTAAACG CTGTGGTGGG AACTGTGCCT GTTGTCTCCA CAATTGCAAT GAATGTCAAT
 +3 C V P S K V T K K Y H E V L Q L R P K T
 901 GTGTCCCAAG CAAAGTTACT AAAAAATACC ACGAGGTCCT TCAGTTGAGA CCAAAGACCG
 +3 G V R G L H K S L T D V A L E H H E E C
 961 GTGTCAGGGG ATTGCACAAA TCACTACCG ACGTGGCCCT GGAGCACCAT GAGGAGTGTG
 +3 D C V C R G S T G G H H H H H H *
 1021 ACTGTGTGTG CAGAGGGAGC ACAGGAGGAC ATCATCACCA TCACCATTGA TCTAGAGTCG
 1081 ACCTGCAGGC AAGCTT

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Figure 22. Disulphide-linked dimerisation of VEGF-X

(A) Mammalian cell expression



(B) *E.coli* expression

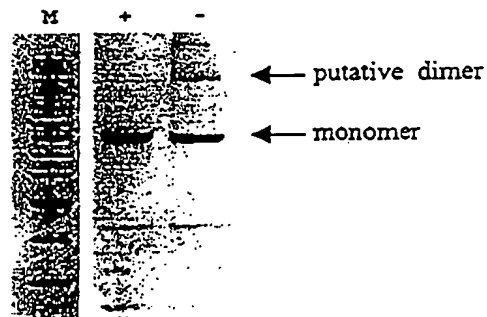


Figure 23. Glycosylation of VEGF-X

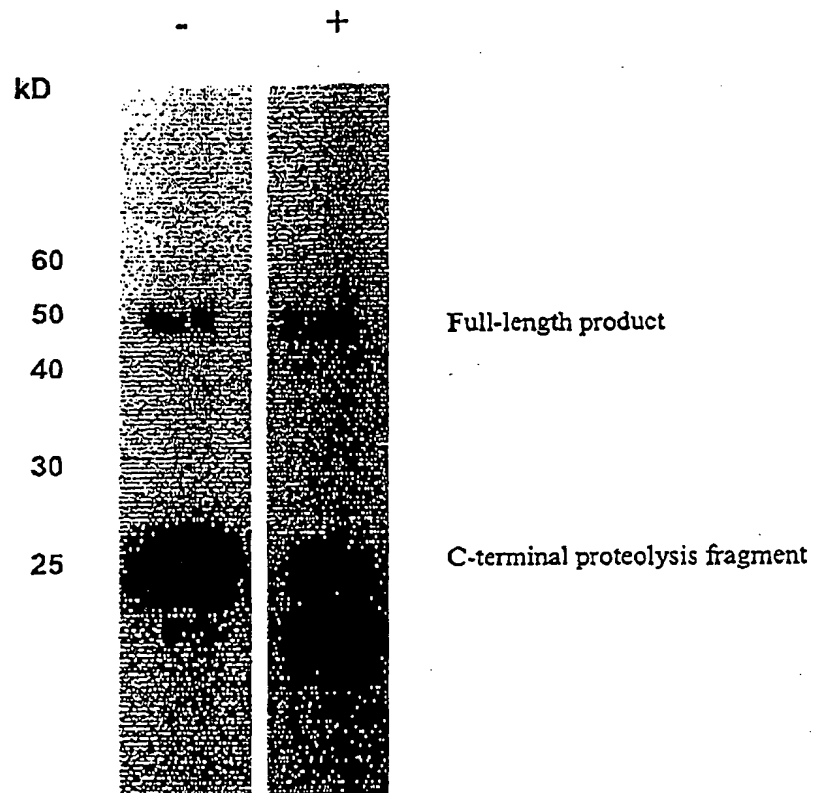


Figure 24. DNA and polypeptide sequence used for *E.coli* expression of the PDGF-like domain

```

+3      M R G S H H H H H H G M A S M
1  AAGGAGATAT ACATATGCCG GGTTCATC ATCATCATCA TCATGGTATG GCTAGCATGA

+3  T G G O O M G R D L Y D D D D K D R G R
61  CTGGTGGACA GCAATGGGT CGGATCTGT ACGACGATGA CGATAAGGAT CCGGGAAGAA

+3  K S R V V D L N L L T E E V R L Y S C T
121 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC

+3  P R N F S V S I R E E L K R T D T I F W
181 CTCGTAACCT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC

+3  P G C L L V K R C G G N C A C C L H N C
241 CAGGTTGTCT CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA

+3  N E C Q C V P S K V T K K Y H E V L Q L
301 ATGAATGTCA ATGTGTCCCA AGCAAAGTTA CTAAAAATA CCACGAGGTC CTTCASTTGA

+3  R P K T G V R G L H K S L T D V A L E H
361 GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

+3  H E E C D C V C R G S T G G
421 ATGAGGAGTG TGAAGTGTG TGCAGAGGGA GCACAGGAGG ATAATGAATT CGAAGCTTGA

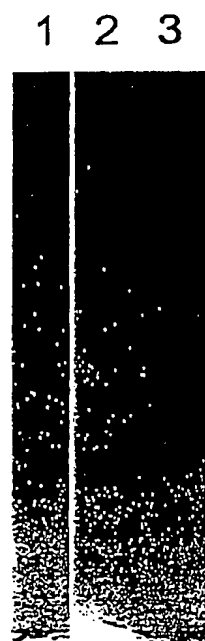
481 TCCGGCTGCT AACAAAGCCC

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Figure 25. Expression of PDGF domain in *E.coli*



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Figure 26. DNA and polypeptide sequence used for *E.coli* expression of the CUB-like domain

```

+2   M A M D I G I N S D P E S H H H H H H
1   G G C G A T G G C C A T G G A T A T C G G A A T T A A T T C G G A T C C G G A G T C T C A C C A T C A C C A C C A T C A

+2   E S N L S S K F Q F S S N K E Q N G V Q
61  T G A A T C C A A C C T G A G T A G T A A A T T C C A G T T T T C C A G C A A C A A G G A A C A G A A C G G A G T A C A

+2   D P Q H E R I I T V S T N G S I H S P R
121 A G A T C C T C A G C A T G A G A G A A T T A T T A C T G T G T C T A C T A A T G G A A G T A T T C A C A G C C C A A G

+2   F P H T Y P R N T V L V W R L V A V E E
181 G T T T C C T C A T A C T T A T C C A A G A A T A C G G T C T T G G T A T G G A G A T T A G T A G C A G T A G A G G A

+2   N V W I Q L T F D E R F G L E D P E D D
241 A A A T G T A T G G A T A C A A C T T A C G T T T G A T G A A A G A T T T G G G C T T G A A G A C C C A G A A G A T G A

+2   I C K Y D F V E V E E P S D G T I L G R
301 C A T A T G C A A G T A T G A T T T T G T A G A A G T T G A G G A A C C C A G T G A T G G A A C T A T A T T A G G G C G

+2   W C G S G T V P G K Q I S K G N Q I R I
361 C T G G T G T G G T T C T G G T A C T G T A C C A G G A A A C A G A T T T C T A A A G G A A A T C A A A T T A G G A T

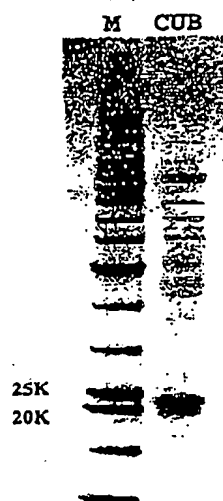
+2   R F V S D E Y F P S E P G F C I H Y N I
421 A A G A T T T G T A T C T G A T G A A T A T T T C C T T C T G A A C C A G G G T T C T G C A T C C A C T A C A A C A T

+2   V M P Q F T E A V
491 T G T C A T G C C A C A A T T C A C A G A A G C T G T G T A G T C G A G C T C C G T C G A C A A G C T T G C G G C C G C

541 A C T C G A G C A C

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Figure 27. Expression of the CUB domain in *E.coli*



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Figure 28. The Effect of Truncated VEGF-X (CUB domain) on HUVEC Proliferation

(A)

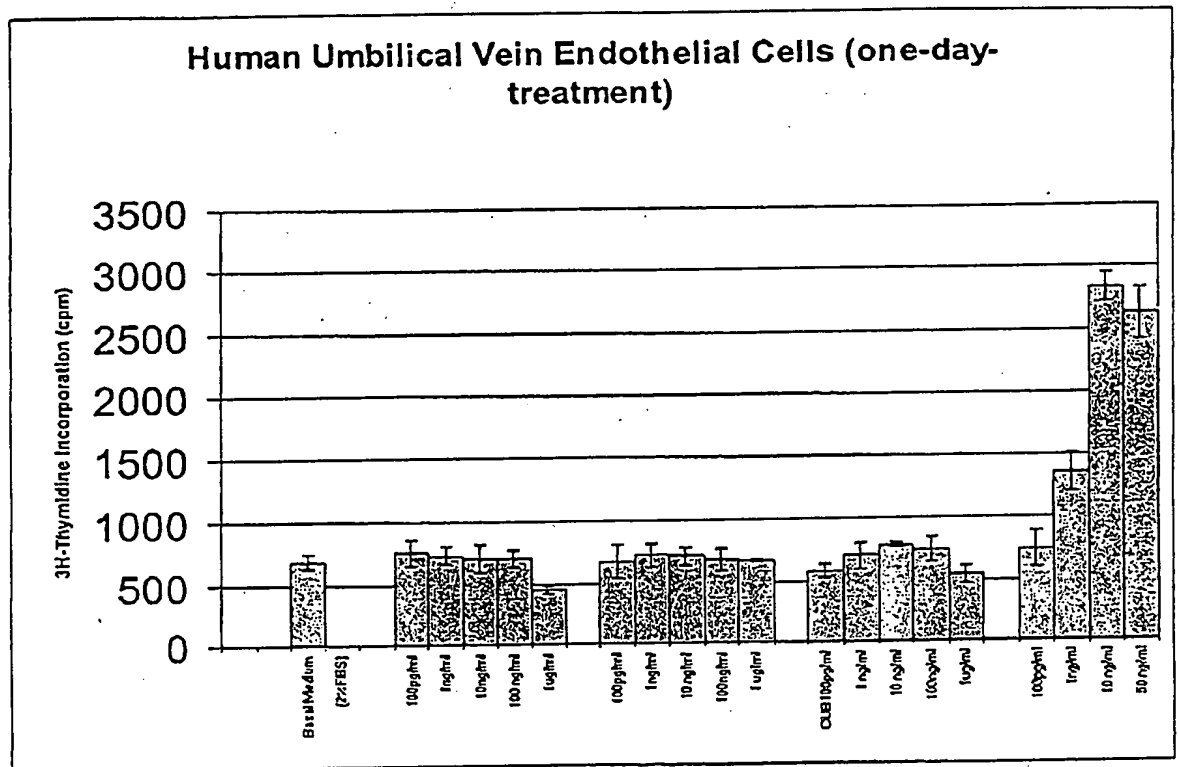
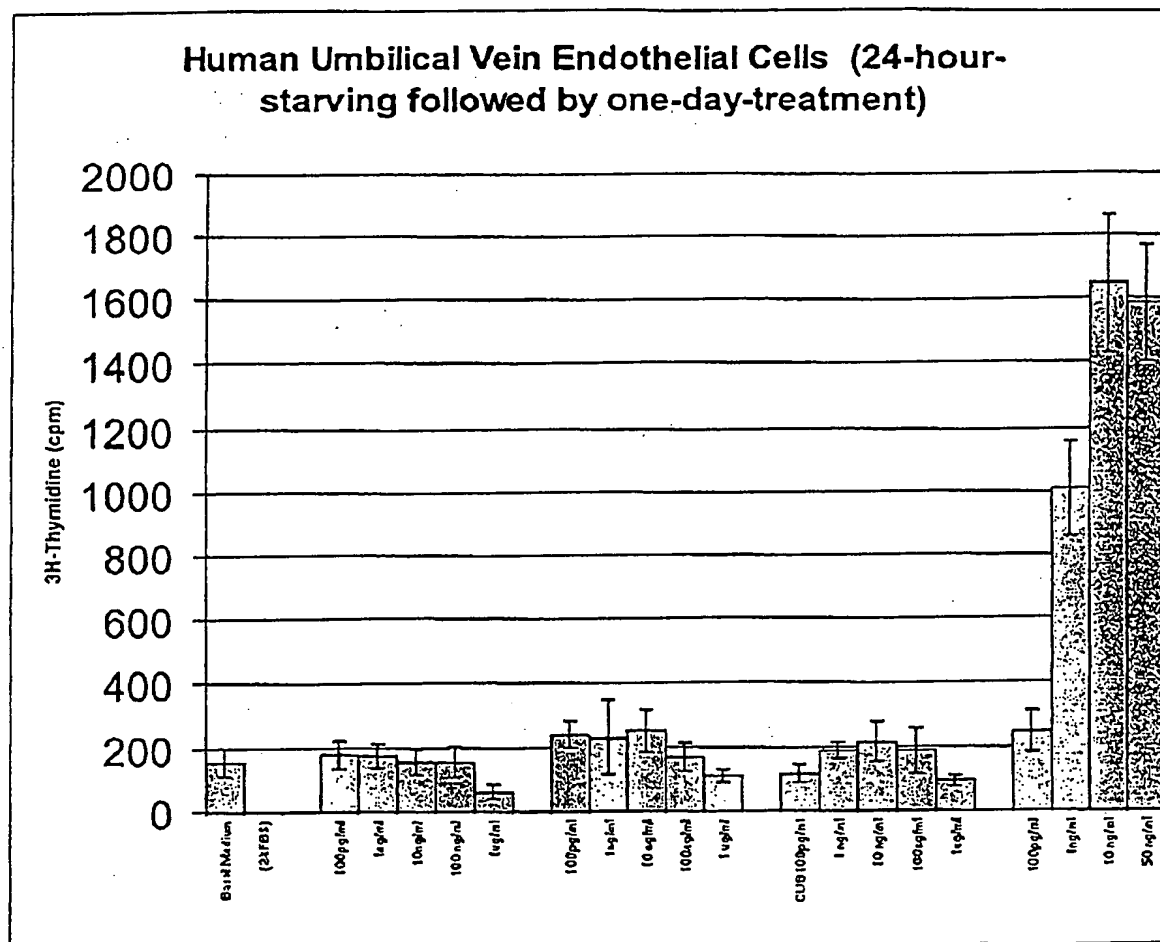


Figure 28 Continued

(B)



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Figure 28

(C)- The effect of VEGF-A₁₆₅ and VEGF-X CUB domain on the proliferation of HUVEC (two-day-treatment).

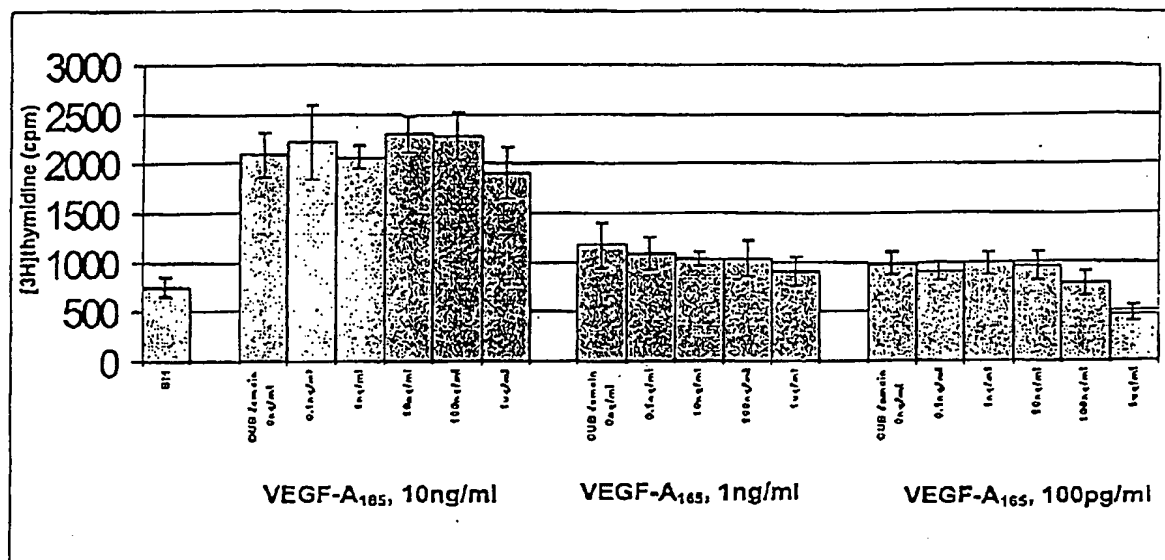
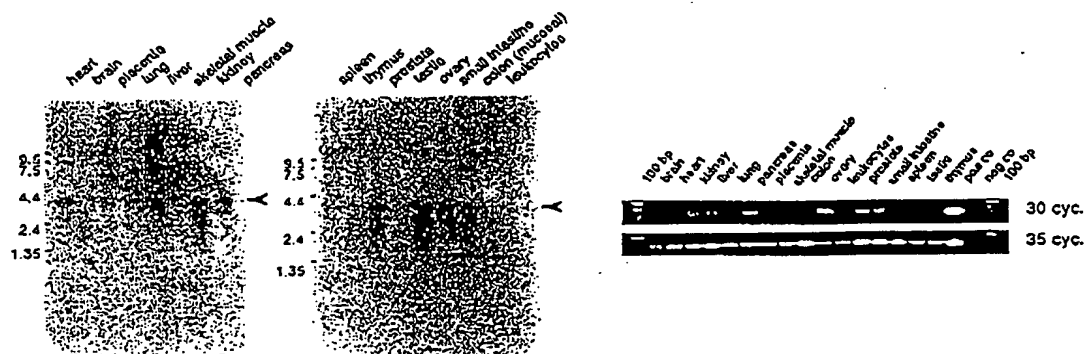


Figure 29 Tissue distribution of mRNA

(A) - Normal tissues



(B) - Tumour tissue and cell lines

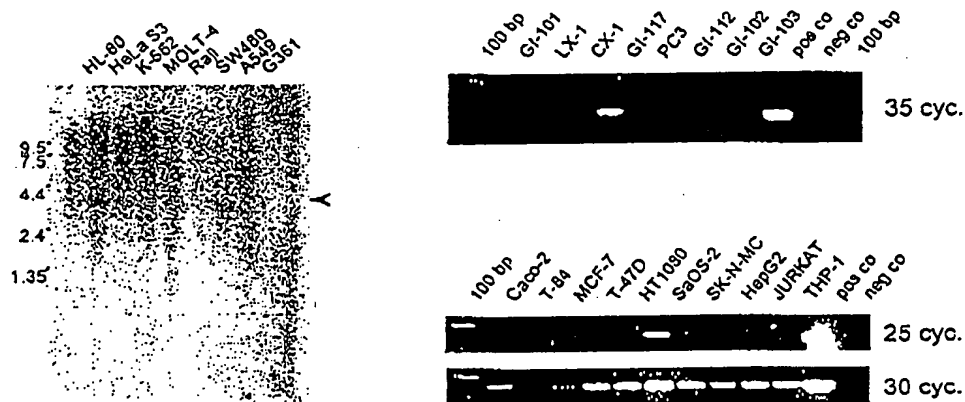


Figure 30. Partial intron/exon structure of the VEGF-X gene

(A) - Genomic DNA sequences of 2 exons determined by sequencing

tttcttttataccatatagtggtggatctgaaccagGGTTCGTCATCCACTACAACATTGTTCATGCCACAATTCACAGAAGCTGTG
AGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGACCTTAT
TCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT
TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTG
TCCATAAGGGAAGAACTAAAGAGAACCATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCGCTG
TTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAATACCACGAGtaggtatacaattttctttttt
ggtttctctcggtattttatgtctt

aaagccagtcataagacattcgttgatttttaaaagtgggttactcttattccctttcagGTCTTCAGTTGAGACCAAAGACCGGT
GTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGG
ATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCAT
CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAAATTAG
GAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCATAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAAGAAAATTAAATGTTGTATT
AAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCCGATACGGCTTAG
GGTAATGTCAAGTACAGGAAAAAACTGTGCAAGTGAACCTGATTCCGTTGCCTTGGCTTAACTCTAAAGCTCCATGTCCTGGGC
CTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGGCGCATATTCACATATGTAAACCAGAACATTCTATGTAATAACCA
TGTTTTTTAAAAAGGAATATGTTGCTATGAATTAAGTTGTGTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAA
AATTTCTGCCATTTAGAAGAAGAGAACTACATTCAATGTTTGAAGAGATAAACCTGAAAAGAGAGTGGCCTTATCTTCACTTTA
TCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTGTGTA
AATATATCTATTTTACCAAAGGTATTTAATATCTTTTTTATGACAACTTAGATCAACTATTTTAGCTTGGTAAATTTTTCTAA
ACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTTCACTTCTCGTATGGTG
CTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTA
TCATATCTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTAGATCCAGCCATTACTAACCTAT
TCCTTTTTTGGGGAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTG
TGCTGTGCAGTAGGAACACATCCTATTTATTGTGATGTTGTGGTTTTATTATCTTAACTCTGTTCCATACACTTGATAAATACA
TGGATATTTTATGTACAGAAGTATGTCTCTTAACAGTTCACTTATTGTAATCTGGCAATTTAAAGAAAATCAGTAAATATTT
TGCTTGTAATATGCTTAATATCGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAGAAATGT
GGCTATTTTGGGAGAAAATTatgtgtgtgtgtgtcgaagattttattcttggactctgagaaaatgaaagataaa

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Figure 30 continued

(B) - Location of splice sites within the cDNA sequence

1 GAATTCGCCC TTTTGTAA ACCTTGGGAA CTGTTTCAGG TCCAGGTTTT GCTTTGATCC
61 TTTTCAAAAA CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT
121 GGAAACTACC CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCAC CCCAGTGCAG
181 CCTTCCCCTG GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCGCCGTG
+3 M S L F G L L L L T S
241 AGTGAGCTCT CACCCAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG
+3 A L A G Q R Q G T Q A E S N L S S K F Q
301 CCCTGGCCGG CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCCAGT
+3 F S S N K E Q N G V Q D P Q H E R I I T
361 TTTCCAGCAA CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG
+3 V S T N G S I H S P R F P H T Y P R N T
421 TGCTACTAA TGGAAGTATT CACAGCCCAA GGTTTCTCA TACTTATCCA AGAAATACGG
+3 V L V W R L V A V E E N V W I Q L T F D
481 TCTTGGTATG GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACCTT ACGTTTGATG
+3 E R F G L E D P E D D I C K Y D F V E V
541 AAAGATTGG GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTAGAAGTTG
+3 E E P S D G T I L G R W C G S G T V P G
601 AGGAACCCAG TGATGGAACCT ATATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA
+3 K Q I S K G N Q I R I R F V S D E Y F P
661 AACAGATTTC TAAAGGAAAT CAAATTAGGA TAAGATTGT ATCTGATGAA TATTTTCTTT
+3 S E P G F C I H Y N I V M P Q F T E A V
721 CTGAACCAAG GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA
+3 S P S V L P P S A L P L D L L N N A I T
781 GTCCTTCAGT GCTACCCCTC TCAGCTTTC CACTGGACCT GCTTAATAAT GCTATAACTG
+3 A F S T L E D L I R Y L E P E R W Q L D
841 CCTTTAGTAC CTTGGAAGAC CTTATTCGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT
+3 L E D L Y R P T W Q L L G K A F V F G R
901 TAGAAGATCT ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGT TTTGGAAGAA
+3 K S R V V D L N L L T E E V R L Y S C T
961 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGT AAGATTATAC AGCTGCACAC
+3 P R N F S V S I R E E L K R T D T I F W
1021 CTCGTAACTT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTCTGGC
+3 P G C L L V K R C G G N C A C C L H N C
1081 CAGGTGTCT CTTGGTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA
+3 N E C Q C V P S K V T K K Y H E V L Q L
1141 ATGAATGTCA ATGTGTCCA AGCAAAGTA CTAATAATA CCACGAGTCT CTCAGTTGA

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+3 R P K T G V R G L H K S L T D V A L E H
 1201 GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC
 +3 H E E C D C V C R G S T G G
 1261 ATGAGGAGTG TGA CTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC
 1321 AGCTCTTGCC CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT
 1381 CTCCATCCTT AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC
 1441 ATTCTGAAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT TTTGAGAGGA
 1501 GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAG AAAATTAAAT GTTGTATTAA
 1561 ATAGATCACC AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTCTGTAT
 1621 TTCAGTTCTT TCGATACGGC TTAGGGTAAT GTCAGTACAG GAAAAAACT GTGCAAGTGA
 1681 GCACCTGATT CCGTTGCCCT GCTTAACTCT AAAGCTCCAT GTCCTGGGCC TAAAATCGTA
 1741 TAAAATCTGG ATTTTTTTTT TTTTTTTTG CTCATATTCA CATATGTAAA CCAGAACATT
 1801 CTATGTACTA CAAACCTGGT TTTTAAAAG GAACTATGTT GCTATGAATT AACTTGTGT
 1861 CATGCTGATA GGACAGACTG GATTTTTCAT ATTTCTTATT AAAATTTCTG CCATTTAGAA
 1921 GAAGAGAACT ACATTCATGG TTTGGAAGAG ATAAACCTGA AAAGAAGAGT GGCCTTATCT
 1981 TCACTTTATC GATAAGTCAG TTTATTGTT TCATTGTGTA CATTTTTATA TTCCTCTTTT
 2041 GACATTATAA CTGTTGGCCT TTCTAATCTT GTTAAATATA TCTATTTTIA CCAAAGGTAT
 2101 TTAATATTCT TTTTATGAC AACTTAGATC AACTATTTT AGCTTGGTAA ATTTTCTAA
 2161 ACACAATTGT TATAGCCAGA GGAACAAAGA TGATATAAAA TATTGTTGCT CTGACAAAAA
 2221 TACATGTATT TCATTCTCGT ATGGTGCTAG AGTTAGATTA ATCTGCATT TAAAAAAGT
 2281 AATTGGAATA GAATTGGTAA GTTGCAAAGA CTTTTTGAAA ATAATTAAAT TATCATATCT
 2341 TCCATTCTCG TTATTGGAGA TGAAAATAA AAGCAACTTA TGAAAGTAGA CATTCAGATC
 2401 CAGCCATTAC TAACCTATTC CTTTTTGGG GAAATCTGAG CCTAGCTCAG AAAACATAA
 2461 AGCACCTTGA AAAAGACTTG GCAGCTTCCT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA
 2521 CACATCCTAT TTATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTC CATACTTG
 2581 TATAAATACA TGGATATTTT TATGTACAGA AGTATGCTC TTAACCAGTT CACTTATTGT
 2641 ACCTGGAAGG GCGAATTCTG CAGATATC

Fig. 30 (cont.)

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The Effect of FL-VEGF-X on HUVEC Proliferation: (24-hour serum starvation followed by one day- treatment)

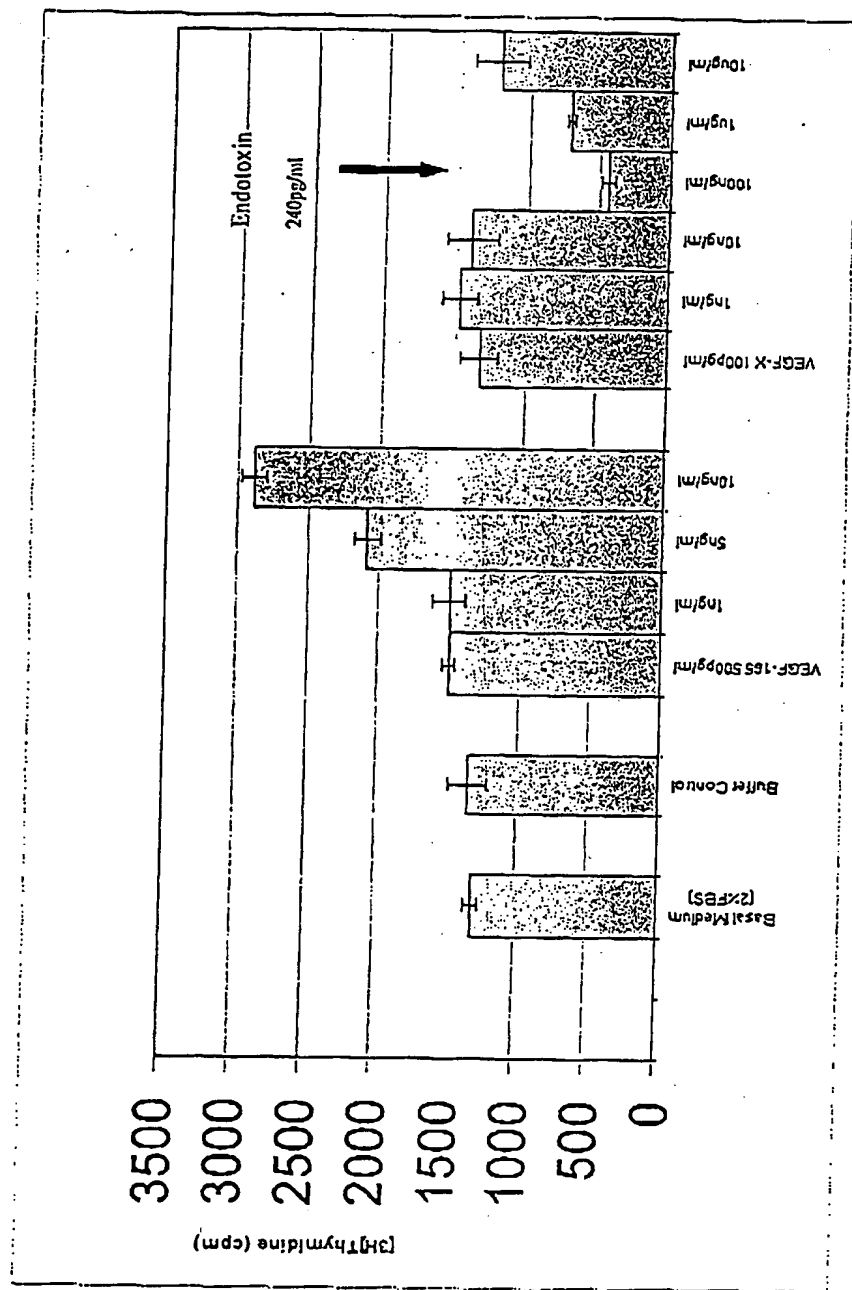


Fig. 31

The Combined Effect of Truncated VEGF-X (CUB domain) and Human Recombinant VEGF₁₆₅ on HUVEC Proliferation: (24-hour serum starvation followed by two-day-treatment)



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The Combined Effect of CUB Domain and Human Recombinant bFGF on HUVEC Proliferation : (24-hour serum starvation followed by two-day-treatment)

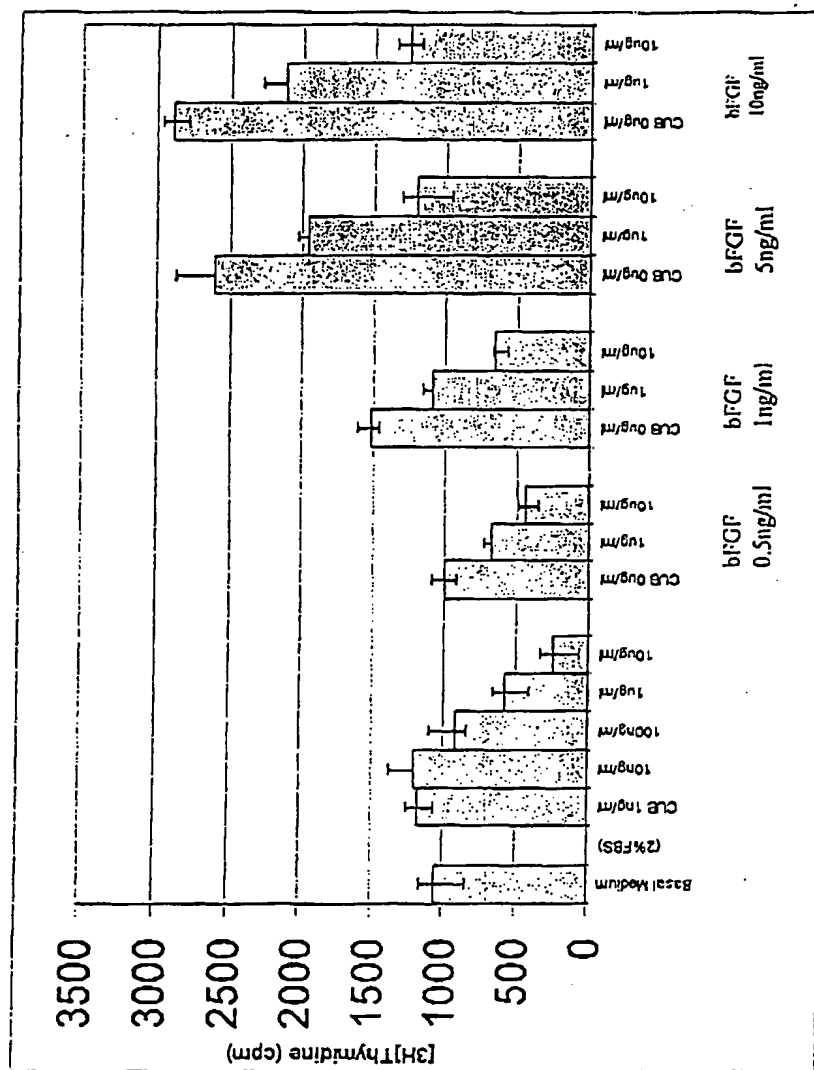
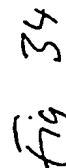


Fig. 33



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LDH Assay for Testing Cytotoxicity of CUB Domain or CUB Domain with rh-bFGF

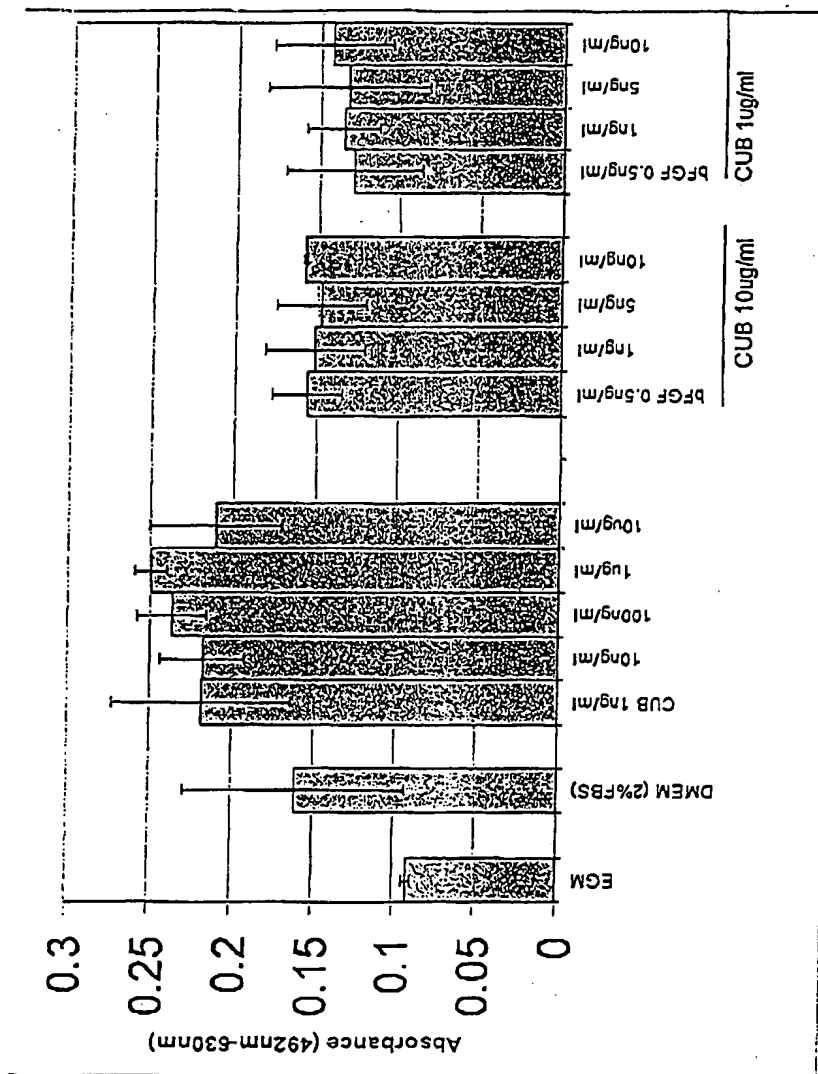


Fig 35

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